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RESULT COPE ACT OF ACT 
RA Adams M.D., Celniker S.E., Helt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dorson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dorson K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Liux X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liux X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
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Ephydroidea; Drosophilidae; Drosophila
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01-OCT-2002
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A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
B Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
A Houanenavong S., Strong R., Svirskas R., Tector C., Tyler D.,
A Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Mount S.M., Moy M., Murphy B., Murphy L., Muzry D.M., Welson D.L.,
A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
A Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.
U Science 287:2185-2195(2000).
                                                                                 Champe M., Chavez C., Dorsett V., Farfan D., Frise E., G
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mung
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: CONTAINS 4 KH DOWAINS.
EMBL; ABO03484; ABAF47958.2; -
EMBL; AF241237; AAF63331.1; -
EMBL; AF241237; AAF63331.1; -
                                                                                                                                                                                                                                                                                                                "Listen J., Nielsen F.C., Christiansen J.; "Cloning and Expression of a Drosophila Homolog of IMP/Vg1-RBP."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
[7]
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                                                   FlyBase; FBgn0030235; Imp.
GO; GO:0003676; F:nucleic acid binding;
                    InterPro;
InterPro;
                                                                                                                                                                                                                                                                       Stapleton M.,
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Submitted (MAR-2000)
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            IPR004087; KH_dom.
IPR004088; KH_type_1.
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Pred. No. 21 the number of results predicted by chance to

KEYWORDS SOURCE

ORGANISM

Unknown

Unknown. AR171867.1

REFERENCE

TITLE AUTHORS

Unclassified.

1 (bases 1 to 3283)
Chen,Y.-T., Gure,A., Tsang,S., Stockert,E., Jager,E., Alexander,K. and Old,L.J.
Isolated mucleic acid molecule encoding cancer associated antigen, the antigen itself, and uses thereof

RESULT 1
AR171867
LOCUS
DEFINITION
ACCESSION
VERSION

AR171867

Sequence 8 from AR171867

patent US

3283

283 bp 6297364.

DNA

linear

PAT 17-DEC-2001

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1 (bases 1 to 3283)
Chen, Y.-T., Gure, A., Tsang, S., and Old, L.J.
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                                           Isolated nucleic acid molecules encoding cancer-associated antigens, these antigens and method of using the same antigens; these antigens and method of using the same LUDWIG INSTITUTE FOR CANCER RESEARCH

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                                                                                                                                                                                                                                                                                                                      Chen, Y.T., Gure, A., Tsang, S., Old, L.J.
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/mol_type="genomic DNA"
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1083 GATAGAGATTATGAAGAAGCTGCGTGAGGCCTTTGAAAATGATATGCTGGCTG			
1023 ATACAHCCCGGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCTGA 1082 	s 2:	/ Match 99.1%; Score 3253.8; DB 9; Length 3667; Local Similarity 99.8%; Pred. No. 0; nes 3277; Conservative 0; Mismatches 3; Indels 2: Gaps	Query Match Best Local Matches 327
GAAAATTGAACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCAT	·	DENEEVIVRIIGHFFASQTAQRKIREIVQQVKQQEQKYPQGVASQRSK"	ORIGIN
963 GAAAATTGAACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCAT 1022	RAQGRIF Qy	TOAVGAIIGKKGAHKKOLARFAGASIKLARFAGROTIGKGGKTVNELQNIJTSAEVIVPROOTP GKLKEENFFNPKEEVKLEAHIRVPSSTAGRVIGKGGKTVNELQNIJTSAEVIVPROOTP	
903 AATCTTGGCACACAATGGCTTGGTTGGAAGACTGATTGGAAAAGAAGGAAG	EGLTIKN Qy KLAEEIP KGTVEAC Db	SSPSPPQRAQRGDHSSREQGHAPGGTSQARQIDFPLRILVPTQFVGAIIGKEGLTIKN ITKQTQSRVDIHHRKENSGAAEKPVTIHAPPEGTSBACRMILEIMQKEADETKLAEEIP LKILAHNGLVGRLIGKEGRNLKKIEHETGKTITSSLQDLSIYNEERTITVKGTVBAC AAARITMAKKILTAAFENNMIANTHSCOVESSIVOOHHOODINGKTIKKIITKEEL	
843 TCTTGAAATCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAA 902 	GYAFVD EVLDGLL TIPDEEV O O O O O O O O O O O O O	/ UD_XTEI="151:4883681" / translation="MMNKLYIGNLSPAVTADDLRQLFGDRKLPLAGQVLLKSGYAFVD YPDQNWALIAAIETLSGKVELHGKIMEVDYSVSKKLRSRKIQIRNIPPHLQWEVLDGLL AQYGTVENVEQVNTDTETAVVNVTYATREEAKIAMEKLSGHQFENYSFKISYIPDEEV	
	Db		
	O _V Lb	/gene="p62" /note="RNA-binding protein"	1
CATCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAAGAGAACTCTGGAGCTGC	. Q	1. 3667 /gene="p62" 436	gene
1029 CCTGGTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGAA 722	ממ	/or /mo /db	
GCAAGGCCACGCCCCTGGGGGCACTTCTCAGGCCAGACAGA	? <u></u>	I	FEATURES source
603 GCAAGGCCACGCCCCTGGGGGGGCACTTCTCAGGCCAGACAGA	The Qy Jolla,	1998) Molecular & Experimental Medicine, Institute, 10550 N. Torrey Pines Road, La	JOURNAL
543 AGAGGTGAGCTCCCCTTCGCCCCCTCAGCGAGCCCAGCGGTGGGGACCACTCTTCCCCGGGA 602	Qγ	2 (bases 1 to 3667) 2 (bases 1 to 3667) 2 hang, J.Y., Chan, E.K.L., Peng, X.X. and Tan, E.M. Direct Submission	REFERENCE AUTHORS TITLE
	Db	gen in human hepatocellular carcinoma Med. 189 (7), 1101-1110 (1999)	JOURNAL MEDLINE
n oo	OV 5	Zhang, J.Y., Chan, E.K., Peng, X.X. and Tan, E.M. A novel cytoplasmic protein with RNA-binding motifs is an	AUTHORS TITLE
AGAAACCGCCGTTGTCAACGTCACATATGCAACAAGAAGAAGAAGAAAAAATAGCCATGGA	• •	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 3667)	REFERENCE
363 GGATGGACTTTTGGCTCAATATGGGACAGTGGAGAATGTGGAACAAGTCAACACAGACAC 422 	do Vy		KEYWORDS SOURCE ORGANISM
	mRNA, Db	Homo sapiens hepatocellular carcinoma autoantigen (p62) complete cds. AF057352	ACCESSION ACCESSION
CTCGGGTAAAGTGGAATTCCATGGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAAAA 3		D D	RESULT 4 AF057352 LOCUS
103 COSCIACOCCITICOINGACIACCECGACAGAACIGGGCCATCGCGCCATCGAGACCCT 242	סם סלם	3241 CCNATATGGCCTTCTTTTGGACAAACCTTGAAAATGTTTATTT 3283 	Qy 3 3 3
CCTCCGGCAGCTCTTTGGGGACAGGAAGCTGCCCCTGGCGGACAGGTCCTGCTGAAGTC	3240	3181 GAGAAGGTGACAGTCCAAGTGTGCAACAGCTGTTCTGAATTGTCTTCCGCTAGCCAAGAA 	Qy 3 Db 3
	3180	3121 TTTTTTATTTTTTAATAAAATGAGTTGGAAAAAAAATAAGATATCAACTGCCAGCCTG	Qу 3 ДЬ 3
	3120	3061 CCTCAGCACCTTGCTCTTGTGTTTCCCTTAGAGATTTTGTAAAGCTGATAGTTGGAGCAT 	Qy 3 Db 3

2349 CTGCAGCCTTCAGCTATCCACTTCACCTCGGATCTTTTAGTTGAACTCCACCAGCCAG	69 29 23 89		43 03 69 63	
3122 3488 3182 3548 3548 3242 3608	Qy 2943 T-AAAAAAAAATGTGGAGGAAAGTAGAAATTTACCAAGGTTGTTGGCCCAGGGCGTTA Db 3308 TAAAAAAAAAAATGTGGAGGAAAGTAGAAATTTACCAAGGTTGTTGGCCCAGGGCGTTA Db 3308 TAAAAAAAAAAAATGTGGAGGAAAGTAGAAATTTACCAAGGTTGTTGGCCCAGGGCGTTA Db 3308 TAAAAAAAAAAAAATGTGGAGGAAAACACACAGAAGAAGTACCTCAGGTGTTTTAC Qy 3002 AATTCACAGATTTTTTAACGAGAAAAACACACAGAAGAAGCTACCTCAGGTGTTTTTAC Db 3368 AATTCACAGATTTTTTTAACGAGAAAAAACACACAGAAAGAA	Db 3068 ĀTĊĀĊĀTĊĀCĀĀĀĀĀĞĞĀACĀĀĀĀGGĀĀĀCACACACACACACACACTTACACTTGG Qy 2763 TTACTCAAĀĀGĀACĀĀĀĀGGTCAĀTGGTĀCTTGTCCTĀGGĀĀĀGĀĀĀGGĀĀĀĀCĀGĀ Db 3128 TTACTCAĀĀĀGĀĀCĀĀĀGĀGTCAĀTGGTĀCTTGTCCTĀGGGTTTTGGĀĀĀĀĀGĀĀĀACĀGG Db 3128 TTACTCAĀĀĀGĀĀCĀĀGĀĀGTCĀĀTGTĀCTCTCTĀGCGTTTTGGĀĀĀĀĀĀĀGĀĀĀTGTĀT Qy 2823 ĀĀCCCĀĀCCĀĀĀCCĀĀTCĀĀCCĀĀĀGĀĀĀĀĀĀTTCCĀCĀĀĀTGĀĀĀGĀĀTGTĀT Db 3188 ĀĀCCCĀCĀĀĀCCĀĀĀCCĀĀTCĀĀCCĀĀĀGĀĀĀĀĀTTCCĀCĀĀĀTGĀĀĀGĀĀĀ		Db 2529 AAGATATGTGGCCTGTGGGTTACACAGGGTGCCTGCAGCGGTAATATATAT

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CTCGTCGGAAGGAAACTCACGGCAGTTCTCGATCCTCCTCCATCCCCAAAGCCAAACCACAAACCACCACAAACCACAAAACCACAAAACCACA	212 341 341 272 272 272 2401 332 3461		1741 ATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCAGGGAA 1800 1672 ATTGTACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGC 1801 ATTGTACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGC 1860 ATTGTACAACAGGTGAAGCAGCAGCAGCAGAAACAACGAAGGAGTCGCCTCCAACAC 1791
TITLE Isolated nucleus encoding cancer associated nucleus the encoding cancer associated nucleus thereof the antigen itself, and uses thereof JOURNAL Patent: US 6576756-A 6 10-JUN-2003; FEATURES	3412 bp DNA linear PAT 17 om patent US 6576756. II:33738476	Qy 3052 GTGTTTTACCTCAGCACCTTCCTCTTTTCCTAGAGATTTTGTAAAGCTGATAG	Qy 2752 CTTACACTTGGTTACTCAAAAGAACAAGAGTCAATGGTACTTGTCCTAGCGTTTTGGAAG 2811 Db 2881 CTTACACTTGGTTACTCAAAAGAACAAGAGTCAATGGTACTTGTCCTAGCGTTTTGGAAG 2940 Qy 2812 AGGAAAACAGGAACCCACCAAACCAACCAAACAAAAAAAA

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2152 GGGAAGATGTTAAGATATGTGGCCTGTGGGTTACACAGGGTGCCTGCAGCGGTAATATAT	2092 AAAATGCACACCCTTTTTCTGTGGCAAATCGTCTCTGTACATGTGTGTACATATTAGAAA 	1 2	2 CCCC	1912 CGAGGAGGGGGGGAAGGTCAGCCAGGTTTGCCAGAACCACCGAGCCCCGCCTCCCGCC	1852 GAATGAGAAGTCTGCGGAGGCGGCCAGGGACTCTGCCGAGGCCCTGAGAACCCCAGGGGC	2	1732 AGCAAGTGAGGCTCCCACAGGCACCAGCAAACAACGATGAATGTAGCCCTTCCAACAC 	1	1612 ATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGAT	1552 TTAACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTG	92 21	32 61	1372 ATCACCGGGCCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAA 	12 41	52 81	92 21	1141ACCCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGTTTGGCCC	1201 CTGTCCGTGCTATCTCCACCAGCAGGGCCCCGCGGAGCTCCCCCCCGCTGCCCCTACCAC

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32 AGCCAAGAACCNATATGGCCTTCTTTTGGACAAACCTTGAAAATGTTTATTT 3283 	3172 GCCAGCCTGGAGAAGGTGACAGTCCAAGTGTGCAACAGCTGTTCTGAATTGTCTTCCGCT 3231	3112 TTGGAGCATTTTTTTTTTTTTTTTTTAAAAATAGAGTTGGAAAAAAA	3052 GTGTTTTTACCTCAGCACCTTGCTCTTGTGTTTCCCTTAGAGATTTTGTAAAGCTGATAG 3111	2992 CAGGGGGTTAAATTCACAGAGTTTTTTTAACGAGAAAAACACACAGAAGAAGCTACCTCAG 3051	2932 ATTCCTTTCTTTAAAAAAAAATGTGGAGGAAAGTAGAAATTTACCAAGGTTGTTGGCC 2991 3061 ATTCCTTTCTTTAAAAAAAAATGTGGAGGAAAGTAGAAATTTACCAAGGTTGTTGGCC 3120	2872 AAAGAATGTATTTTGTCTTTTTTGCATTTTTGGTGTATAAGCCATCAATATTCAGCAAAAATG 2931	2 AGGAAAACAGGAACCCACCAAACCAACCAATCAACCAAACAAA	752 CTTACACTTGGTTACTCAAAAGAACAAGAGTCAATGGTACTTGTCCTAGCGTTTTGGAAG 2811	2692 GTGCTCTGAGTATCACATCACAAAAGGAACAAAAGCGAAACAAAC	2632 TITCCTCATCCCTCCATCTCAATCCCGTATCTACGCACCCCCCCC			CTCGTCGGAAGGACACTCACGGCAGTTCTGGATCACCTGTGTATGTCAACAGAAGGATA CTCGTCGGAAGGACACTCACGGCAGTTCTGGATCACCTGTGTATGTCAACAGAAGGGATA CTCGTCGGAAGGACACTCACGGCAGTTCTGGATCACCTGTGTATGTCAACAGAAGGGATA	TO THE OLD THE ARCHIVE AND COLOR TO THE OLD TH	TETTTCTTTTTTAAAGGAAAGCAGGCTTTTCTAGACTTTAAAGAATAAAGTCTTTGGGAG	
Qy 301 AAGCTAAGGAGCAGGAAAATTCAGATTCGAAACATCCCTCCTCCACCTGCAGTGGGAGGTG 360	30			ACGGATGATGAACAAGCTTTACATCGGGAACCTGAGCCCCGCCGTCACCGCCGAC			/mol_type="genomic_DNA" /db_xref="taxon:9606" ORIGIN	H	ers	PC CIZNI/15, PC C12N1/19,C12N1/21,C12N5/10,C12P21/08,C12Q1/68,G01N33/53,G01N33/ PC C17N1/19,C12N1/21,C12N5/10,C12P21/08,C12Q1/68,G01N33/53,G01N33/ PC	PD 23-APR-2002 PF 16-MAR-1999 UP 2000545030 PF 17-APR-1999 US 09/061709 PR 17-APR-1998 US 09/061709 PI YAO TSENG CHEN, ALI GURE, SOLAM TSANG, ELISABETH STOCKERT, ELKE	≨ <u>o</u> i	nucle:	(Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3412)		DEFINITION Isolated nucleic acid molecules encoding cancer-associated artigens, these antigens and method of using the same.

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                                                                                                               Homo sapiens IGF-II mRNA-binding protein MGC:29539 IMAGE:5090334), complete cds. BC021290
L (Dases 1 to 3033)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E. J., Lu, X., Gibbs, R.A., Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Miting, M., Madan, A., Rodrigues, S., Sanchez, A., Miting, M., Madan, A., Rodrigues, S., Sanchez, A., Blakesley, R.W., Touchman, J.W., Green, E.D., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Generation and monise cDNA seconences
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27552765
Location/Qualifiers
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Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,

Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,B.D.
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On Aug 19, 2003 this sequence version replaced gi:18204200
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
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Tissue Procurement: ATCC
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Proc. Natl. Acad. Sci. U.S.A. S
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                                                                                                                                                              GCTAAGCGGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGATGAAGA
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                                             CAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGT
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677 ACAACAGGTGAAGCAGCAGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAA 173	677 ACAACAGGTGAAGCAGCAGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCACAA 173 801 ACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAA 173 801 ACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAA 186 737 GTGAGGCTCCCACAGGCACCAGCAAAACAACGATGAATGTAGCCCTTTCCAACACCTGAC 179
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677 ACAACAGGTGAAGCAGGAGCAGAAATACCCTCAGGGAGTCACCAGGCGAGCAA 1734	677 ACAACAGGTGAAGCAGAGCAGAACTACCTCAGGGAGTCGCCTCACAGCGCAGCAA 1734 801 ACAACAGGTGAAGCAGCAGAGCAGAACTACCCTCAGAGGAGTCGCCTCACAGCGCAGCAA 1734 801 ACAACAGGTGAAGCAGAGCAGAGAATACCCTCAGAGGATCGACTCCACAGCGCAGCAA 1861 802 ACAACAGGTGAAGCAGAACAACAACCGCAGAGCAGCAGCAGCAGCAGCA
677 ACAACAGGTGAAGCAGCAGAGCAGAAATACCCTCAGGGAGTCACAGGCCAACACCAGCAACACCAGGCAACACCAGACAACA	677 ACAACAGGTGAAGCAGGAGCAGAACTACCTCAGGGAGTCGCCTCACAGCGCAACAGCAA 1734 801 ACAACAGGTGAAGCAGCAGGAGCAGAATTACCCTCAGGGAGTCGACAGCGCAACAGCGAACAGCAA 1734 802 ACAACAGGTGAAGCAGAGAGAGAGAATTACCCTCAGAGGAGTCGACACACCCTGACAGCGAGCAAAACAACAGCAGAAATTACCCTCAGAGAGTGAATGAGCCCTTCCAACACCCTGAC 1861 803 GTGAGGCTCCCACAGGCACCAGCCAAAACAACGAGATGAATGA
677 ACAACAGGTGAAGCAGAAGCAGAAATACCCTCAGGGAGTCTCCACAGGCCAACACTACTACAACAGGTGAAGCAAGC	677 ACAACAGGTGAAGCAGGAGCAGGAGCAGAATACCCTCAGGGAGTCGCCTCACAGCGCAACAGCAA 1731 801 ACAACAGGTGAAGCAGCAGGAGCAGAATACCCTCAGAGGTCGCCTCACAGCGCAGCAA 1731 801 ACAACAGGTGAAGCAGGAGGAGCAGAAATACCCTCAGAGGAGTGAATGCCTCACAGGCCAGCAACACCCTGAC 1861 802 ACAACAGGTGAAGCAGCAGAGAAATACCCTCAGAGGATGAATGTAGCCCTCACAGCCCAGCAGCAACACCCTGAC 1861 803 GTGAGGCTCCCACAGGCACCAGCCAGAAACAACGAAGACCAAAGACCAACACCCTGAC 1921 804 GTGAGGCTCCCACAGGCAGCCAGCCAGATGAATGTAGCCAAAGACCATCTGAGGAATG 1922 805 AGAATGAGACCAAAACGCAGCCAGGCCAGATGGGAGCCAAACCCAAGAACCCAACACCCTGAC 1921 805 AGAAGTCTGCGGAGGCGAGCCAGGACTCTGCCGAGGCCCTGAGAACCCCAGGGCCCAGG 805 AGAAGTCTGCGGAGGCCAGGCCAGGATTCTGCCGAGGCCCTGAGAACCCCAGGGCCCAGG 191 806 AGAAGTCTGCGGAGGCGAGGCCAGGACTCTGCCGAGAACCCCAGGGCCCAGGGCCCAGG 807 AGAAGTCTGCGGAAGGTCAGCCAGGGACTTTGCCAGAACCCCCAGGGCCCCCCAGGGCCCCCCA 807 AGAAGTCTGCGGAAAGGTCAGCCAGGGACTTTGCCAGAACCCCCAGGGCCCCCCAGGGCCCCCCA 808 AGAAGTCTGCGGAAAGGTCAGCCAGGGACTTTGCCAGAACCCCCGAGGCCCCCCCAGGGCCCCCCA 809 AGAAGTCTGCGGAAAGGTCAAGCTAGCCAGAACCCCCGCCCCCCAAACTCCACTTCAGCCAAGACCCCCCCC
677 ACAACAGGTGAAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGGCAGCAA 1734	677 ACAACAGGTGAAGCAGAGCAGAGCAGAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAA 1734
677 ACAACAGGTGAAGCAGCAGAGCAGAAATACCCTCAGGGAGTCTCCACAGGCCAGCAA 1734	677 ACAACAGGTGAAGCAGGAGCAGAACTACCCTCAGGGAGTCGCCTCACAGCGCAACAGCAA 1734
	677 ACAACAGGTGAAGCAGGAGCAGAACTACCCTCAGGGAGTCGCCTCACAGCGCAACTACAGCGCAACTACAGCGCAACTACAGCGCAACTACAGCGCAACTACAGCGCAACTACAGCGCAACTACAGCGCAACTACAGCGCAACTACAGCGCAACTACACAGCGAACTACACAGCGAACTACACAGCAACAACTACACCACAGCAACAACACCAACAACCAAC
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677 ACAACAGGTGAAGCAGGAGCAGAAATACCCTCAGGGAGTCTCCACAGCGCAGCAA 1731	677 ACAACAGGTGAAGCAGGAGCAGGACCAGAATACCCTCAGGGAGTCGCCTCACAGCGCAACAGCAA 1734
677 ACAACAGGTGAAGCAGAAGCAGAAATACCCTCAGGGAAGTCGCCTCACAGGGCAGCAA 1734	677 ACAACAGGTGAAGCAGGAGCAGGAGCAGAATACCCTCAGGGAGTCGCCTCACAGCGCAACAGCAA 1731
677 ACAACAGGTGAAGCAGGAGCAGAAATACCCTCAGGGAGTCTCCACAGCGCAGCAA 1734 801 ACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAA 1734 802 ACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAA 1866 803 ACAACAGGTGAAGCACAGCAGCAGAAAACAACCACTGAGCGCAGCAA 1866 804 ACAACAGGTGAAGCACAGCAGCAGAAAACAACCACTGAGCCCTCCACACCCTGAC 1867 737 GTGAGGCTCCCACAGCCAGCCAGAAACCAAACCGATGAACTTAGCCCTTCCAACACCTGAC 1794 865 GTGAGGCTCCCACAGCCAGCCAGAAACCAAACCGAAACCCAAACACCTGAC 1924 961 AGAATGAGACCAAACGCAACCCAGCCAGATCGGGAGCAAAACCAAAACCCAAACACCATGAC 1924 981 AGAAGTCTGCGGAGGCGAGCCAGGCCAGATCCGGAGCCCTGAGAACCCCAGGGGCCGAGG 1914 981 AGAAGTCTGCGGAGGCGGCCAGGCCAGGCCTCGGAGGCCCTGAGAAACCCCAGGGGCCGAGG 1914 981 AGAAGTCTGCGGAGGCGAGCCAGGGAACCCCCAGGGGCCCCAGGGGCCCAGGGCCCCAGGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGAACCTCCCCCCAGGGCCCCCAGGAACCTCCCCCCAGGGCCCCCCAGGAACCTCCCCCCCC	677 ACAACAGGTGAAGCAGAGCAGAACTACCTCAGGGAGTCGCCTCACAGCGCAACTACTACAACAGGTGAACTACAGAGTGAACAGGTGAACAGGGAACAGCAACAGGTGAACAGGGAACAGCAACAGGTGAACAGGAACAGAGAAACAACAGGTGAAGCAGAAAACAACAGGAAAACAACAGGAACACCTGACACCCTGACACCCTGACACCCTGACACCCTGACACACCCTGACACACCCTGACACACCCTGACACCCTGACACCCTGACACCCTGACACCCTGACACCCTGACACCCTGACACCCTGACACACCCAGACACACCAGACACACAC
677 ACAACAGGTGAAGCAGCAGAGCAGAAATACCCTCAGGGAGTCTCCACAGCGCAGCAA 1734	677 ACAACAGGTGAAGCAGGAGCAGGACCAGAATACCCTCAGGGAGTCGCCTCACAGCGCAACAGCAA 1734 801 ACAACAGGTGAAGCAGCAGGAGCAGAATACCCTCAGAGGAGCACAGCAA 1734 802 ACAACAGGTGAAGCAGAGAGAGAAATACCCTCAGAGGAGTCGACACCCCGCACACACCCGGAGCAGCAGCAGAAATACCCCTCAGAGGAGTGAATGAGCCCTCCACAGCCCAGCACACCCTGACACCCTGACACCCTGACACCCTGACACCCTGACACCCTGACACCCTGACACCCTGACACCCTGACACCCTGACACCCCGACCAGCACACACCCAGCCAG
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677 ACAACAGGTGAAGCAGGAGCAGAAATACCCTCAGGGAGTCTCCACAGGCGAGCAA 1731	677 ACAACAGGTGAAGCAGAGCAGAGCAGAATACCCTCAGGGAGTCGCCTCACAGCGCAACAGCAA 1734 801 ACAACAGGTGAAGCAGCAGAGCAGAATACCCTCAGAGGTCGCCTCACAGCGCAAGCAA
677 ACAACAGGTGAAGCAGCAGAGCAGAAATACCCTCAGGGGAGTCACCTCACAGGGCAGCAA 1734	677 ACAACAGGTGAAGCAGGAGCAGGAGCAGAATACCCTCAGGGAGTCGCCTCACAGCGCAACAGCAA 1734 801
677 ACAACAGGTGAAGCAGAAGCAGAAATACCCTCAGGGAAGTCCCCCACAGGGCAACTACTICAGAGCAAAATACCCTCAGGGAAGTCACACAGGTGAACAGGTGAAACAAGTGAAAATACCCTCAGGGAAGTCACACAGGAACAACAGGTGAAGCAGCAGAAAATACCCTCAGGGATGAATGA	677 ACAACAGGTGAAGCAGGAGCAGGAGCAGAATACCCTCAGGGAGTCGCCTCACAGCGCAACAGCAA 1731 801
ACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAA 1734	677 ACAACAGGTGAAGCAGGACCAGGACCAGAAATACCCTCAGGGATGCCCACAGCGAA 1738 801 ACAACAGGTGAAGCAGCAGAACAGAATACCCTCAGGGATGCACAGCGAACAGCAA 1738 802 ACAACAGGTGAAGCAGGAGCAGAAATACCCTCAGGGATGAATGCCCTCACAGCGCAAGCAA
ACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGGGTCGCCTCACAGCGCACAA 1736	677 ACAACAGGTGAAGGAGCAGAACAGAAATACCCTCAGGGAGTGACCCTCAACACCAA 1738 801 ACAACAGGTGAAGCAGCAGCAGCAGAAATACCCTCAGGGAGTGATGATGACACACAC
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ACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAA 1736	677 ACAACAGGTGAAGGAGCAGAACAGAAATTACCTCAGGGAGTGACCCCAACCAGCAGCAA 1738 801 ACAACAGGTGAAGCAGCAGGAAAATACCCTCAGGGAGTGACTCACACCCCCAACACCGCAGCAGCAGCAGCAGCAGCAGCAG
ACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAA 1736	677 ACAACAGGTGAAGGAGCAGAAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAA 1738
677 ACAACAGGTGAAGCAGCAGGAGCAGAATACCCCTCAGGGAGTCGCCTCACAGCCAACCAA	677 ACHACAGGTGHANGCNGCANGAGCAGCANATACCCTCACGGGACTCACAGGGCTCCACAGGGCACAA 1738 801 ACHACHAGGTGHAGCHAGCAGCAAAATACCCTCAGGGACTCACAGGCCACACAA 1738 802 ACHACHAGGTCCCACAGGCACCAGCAAAATACCCTCAGGGATGAATGA
677 ACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCCACAA 1736	677 ACHACAGGTGHANGCNGCANGAGCAGCANATACCCTCACAGGCATCACACGCCACCACACACAA 1738 801 ACACACGGTGHAGCHAGCAGCAGCAAAATACCCTCAGGGATGATGTAGCCTCACAGGCAGCAA 1738 802 ACACACGGTGAGCCACCAGCCAACCCAGCAAAATACCACCTCAGGGATGAATGTAGCCCTCACAGCCAGC
677 ACAACAGGTGAAGCAGCAGGAGCAGAATACCCTCAGGGAGTGGCCTCACAGCCACAA 1736	677 ACAACAGGTGAAGCAGCAGCAGCAGAAATACCCTCAGGGACTCCACAGGCCTCACAGGCCACAAA 1738
677 ACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCCACACACA	677 ACAACAGGTGAAGCAGCAGCAGAAATACCCTCAGGGACTCACCACCACCACACACA
677 ACAACAGGTGAAGCAGAAGCAGAAATACCCTCAGGGAGTGGCCTCACAGGCACAA 1736	677 ACHACAGGTGHANGCNGCAGGAGCAGAANTACCCTCAGGGACTCCACAGCGCCACCACCACACACACAC
677 ACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCCACAA 1736	677 ACAACAGGTGAAGCAGCAGCAGCAGCAATATCCCTCAGGGACTCCACAGCGCCTCCACAGCGCAGCAA 1738 801 ACAACAGGTGAAGCACCAGCAACCAGCAAAATATCCCTCAGGGATGAATGTAGCGCTCACAGCGCAGCAA 1738 802 ACAACAGGTCCCACAGGCACCAGCAAAACAACAACGAATGTAGCCTTACAGGGATTCCAACACCTGAC 1986 803 GTGAGGCTCCCACAGGCCACCAGCCAACCACAGCAAATTACCCTCAGGGATTGAATGTAGCCCTTCCACAGCGCAGCAA 1866 804 GTGAGGCTCCCACAGGCCACCAGCCAGCCAGATGAATGTAGCCATAGACCCTTCCAACACCTGAC 1920 805 AGAATGAACACCCAAACCGCAGCCAGCCAGCCAGATCGAGTCTGACAACCCAAACCAAACCAACC
677 ACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCCACACCACACCACACCACACCACCACCACCACCA	677 AGAACAGGTGAAGCAGCAGCAGCAGAAATACCCTCAGGGACTCCACCACCACCACACACA
677 ACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCACACGCAACCAA 1736	677 ACAACAGGTGAAGCAGCAGCAGCAGAATACCCTCAGGGACTCCACACGCCACCAAAAATACCCTCAGAGGACTCACACGCCACCAAAAATACCCTCAGGGACTCACACGCCACCAAAAACAACAACGAATGAACTCCCTCACAGGCCTCACAGCCACAAAACAACAACGAATGAACTCACCCTCACAGCCCACCACACCCTGACCAAAACAACAACGAATGAACTCACCCTCACAGCCCACACCCTGACCACAGCCACACACCCTGACCACACCCTGACCACACCCTGACCACACCCTGACCACACCCTGACCACACCCTGACCACACCCTGACCACACCCTGACCACACCCTGACCACACCCTGACCACACCCTGACCACCCTGACCACACCCTGACCACACCCTGACCACACCCTGACCACACCCTGACCACACCCTGACCACCCTGACCACACCCTGACCACACCCTGACCACACCCTGACCACACCCTGACCACACCCTGACCACCCTGACACCCACACCCTGACACCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGACCCACCCAAACACCCCAAACACCCCAAACACCCCAAACAC
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677 ACAACAGGTGAAGCAGAGAGAGAGAATTACCCTCAGGGGTGCCCTCACAGGCCACCAA 1736	677 ACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTTGCCTCAACAGCCCACAA 1736 801 ACAACAGGTGAAGCAGCAGGAGCACAAATACCCTCAGGGAGTTGCCCTCAACAGCCCAGCAA 1736 801 ACACAGGTCCCCACAGGCACCAGAAATACCCTCAGGGATTGACTCCCTCACAGCCCACACCTGAC 1966 803 GTGAGGCTCCCCACAGGCACCAGCAAAACAACGGATTGAATTTAGCCCTTCCAACACCTGAC 1976 804 GTGAGGCTCCCCACAGGCACCAGCCAAAACAACGGATTGAATTTAGCCCTTCCAACACCTGAC 1920 805 GTGAGGCTCCCACAGGCACCAGCCAGAACAACGGATTGAATTTAGCCCTTCCAACACCTGAC 1920 806 GTGAGGCTCCCCACAGGCACCAGCCAGATCGGGAGCCAAACCAAAGCAACCTGAC 1920 807 GGAATGAGACCAAACGCAGCCAGCCAGATCGGGAGCCAAACCAAAGACCAACCTGACACCTGACACCTGAC 1920 808 AGAATGAGACCAAACGCAGCCAGCCAGGACCCAGGGCCCTCCCAAGAACCAAAGACCAAAGACCAAAGACCAAAGACCAAAGACCAAAGACCAAAGACCAAAGACCAAAGACCAAAGACCAAAGACCAAAGACCAACCGAAGCCCCCC
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677 ACAACAGGTGAAGCAGAGAGAGAGAATTACCCTCAGGGAGGTGGCCGCCCCACACACA	677 ACAACAGGTGAAGCAGCAGGAGCAGAATTACCCTCAGGGAGTTGCCTCAACAGCCCACAA 1736 801 ACAACAGGTGAAGCAGCAGGAGCAGAAATTACCCTCAGGGAGTTGCCCCCAACAGCCCAGCAA 1736 801 ACACAGGTGAAGCAGCAGCAGAAATTACCCTCAGGGATTGAGTTGAGCCCTCACAGGCAACACTGAC 1940 803 GTGAGGCTCCCCACAGGCACCAGCAGAAACAACGGATTGAATTTAGCCCTTCCAACACCTGAC 1940 804 GTGAGGCTCCCCACAGGCACCAGCCAGAACAACGGATTGAGCCCTTCCAACACCTGAC 1940 805 AGAATGAGACCAAACGCAGCCAGCCAGATCGGGAGCCAAACCAAAACACCCGAACCAAACACCTGAC 1940 807 AGAATGAGACCAAACGCAGCCAGCCAGATCGGGAGCCAAACCAAAACCACCTGAC 1940 807 AGAATGAGACCAAACGCAGCCAGCCAGATCGGGAGCCCAAAGAACCCCAAGGACCATCTGAGGAATTG 1980 808 AGAATGAGCCAAACGCAGCCAGCCAGCCAGATCGGGAGCCCTGAGGACCCAAGCCCAGGGCCCGAGGTTGAGCAAACCAAACCCCAAGGACCCAAGCCCAAGCCCAAGCCCAAGCCCAAGAACCCCAAGGACCCCAAGGACCCCAAGGACCCCAAGGACCCCAAGGACCCCAAGAACCCCAAAGAACCCCAAGGACCCCAAGGACCCCAAGGACCCCAAGGACCCCAAGGACCCCCAAGGACCCCCC
677 ACAACAGGTGAAGCAGAGAGAGAGAATTACCCTCAGGGAGGTCGCCTCACAGGCCACACAA 1736	677 ACAACAGGTGAAGCAGCAGGAGCAGAATTACCCTCAGGGAGTTGCCTCAACAGCCCACA 1736 801 ACAACAGGTGAAGCAGCAGGAGCAAATTACCCTCAGGGAGTTGCCCTCAACAGCCCAGCAA 1736 801 ACACAGGTTCACACAGGCACCAGAAATTACCCTCAGGGATTGAATTTTAATTATTTTTTTT
677 ACAACAGGTGAAGCAGAGAGAGAGAATTACCCTCAGGGAGGTCGCCTCACAGGCCACACAA 1736	677 ACAACAGGTGAAGCAGGAGCAGAATTACCCTCAGGGAGTGCCCCCACAGGCCCACACA 1736 801 ACAACAGGTGAAGCAGCAGGAGCACAAATTACCCTCAGGGAGTGACCTCACAGCCCAGCACA 1736 801 ACACACAGGTCACAAGCACAGCACAAATTACCCTCAGGAGTCGCCTCACAGCCCAGCAA 1860 737 GTGAGGCTCCCACAGGCACAGCACAAACAACGGATGAATTAGCCCTTCCAACACCTGAC 1736 861 GTGAGGCTCCCACAGGCACAGCCAGACAACACGGATTGAGTGTAGCCCTTCCAACACCTGAC 1737 862 GTGAGGCTCCCACAGGCACCAGCCAGAACAACGGGATGAATTAGCCCTTCCAACACCTGAC 1737 863 GTGAGGCTCCCACAAGCCAGCCAGCCAGATTCGGGAGGCAAACCAAAACACCTGAC 1736 864 GTGAGGCTCCCCACAAACGCAGCCAGCCAGATTCGGGAAGCCAAAGCACCTGAC 1736 865 AGAATGAGCAAAACGCAGCCAGCCAGATTCGGGAAGCCCTGACAAAGCCCCAAGGAATTG 1986 867 AGAATGAGCAAAACGCAGCCAGGCCCAGATTCGGGAAGCCCCTGACAAAGCCCCAAGGGACTTGAGCCCAAAGCCCCAAACCCCAACCTGACAACCCCAAACCCCAACCTGACAACCCCAAACCCCAAACCCCAACCTGACCCCAAACCCCCAAACCCCAAACCCCCAAACCCCCAAACCCC
677 ACAACAGGTGAAGCAGAGAGAGAGAATTACCCTCAGGGGGTCGCCTCACAGGCCACACAA 1736 801 ACAACAGGTGAAGCAGGAGAGAACAACTACCTCAGGGAGGTCGCCCAACACCCTCACAGGCAGCAGACAACTACCCTCAGGGAGTCGCCTCACAGCCACACCCTGAGGAGACCAACACCCTCAGGGAGCACCCCCCACAGGCACCAGACAACACCCCTCAGGGAGCCACCCCCCACAGGCACCAGCAAACAACAGGGATGAATTAGACCCTCACACCCTGAC 861 GTGAGGCTCCCCACAGGCACCAGCCAGACAACACGGATGAACCAAAGCACCTGACCTGACACCTGAC 862 GTGAGGCTCCCCACAGGCACCAGCCAGACCAGATCGGAAGCAAACCAAAGCACCTGAC 863 AGAATGAGACCAAACGCAGCCAGCCAGATCGGGAGCCCTGAGAACCAAAGACCAACCTGAC 864 AGAATGAGCCAAACGCAGCCAGCCAGCCAGATCGGGAGCCCTGAGAACCAAAGACCAACCTGAC 865 AGAATGAGCCAAACGCAGCCAGCCAGCCAGATCGGGAGCCCTGAGAACCAAAGACCAACCTGAC 867 AGAAGTCTGCGGAGGCGCCAGCCAGCCAGATCGGGACCCCAAGACCCAAAGACCAACCCCAGGGCCCCAAGGACCCCAAGGCCCCAAGGACCCCAAGGCCCCCAAGGACCCCAAGGCCCCCAAGGACCCCAAACCCCAAACCCCAAACCCCAAACCCCAAACCCC	677 ACAACAGGTGAAGCAGGAGCAGAATTACCCTCAGGGAGTTGGCCTCACAGGCCAGCAA 1736 801 ACAACAGGTGAAGCAGCAGGAGCAAATTACCCTCAGGGAGTTGACTCCAGCCAG
677 ACHACHGETGHANGCAGCHAGHATHACCTTCAGGGAGTGGCCTCACACGCACA 1736	677 ACAACAGGTGAAGCAGGAGCAGAACTACCCTCAGGGAGTGCGCTCAACGGCCAGCAA 1736 801 ACAACAGGTGAAGCAGCAGGAGCAAATACCCTCAGGGAGTGGCCTCACAGGCCAGCAA 1736 801 ACAACAGGTGAAGCACGAGCAGAAATACCCTCAGGGATTGAATGTAGCCCTTCAACACCTGAC 1866 737 GTGAGGCTCCCCACAGGCACCACCACAAACAACGAACGAA
677 ACHACHGETGHANGCAGGHAGCAGHATHACCTTCAGGHACTGACCTCACAGGCAA 1736	677 ACAACAGGTGAAGCAGCAAGACAAATACCCTCAGGGAGTTGGCCTACAGGGCAA 1736 801 ACAACAGGTGAAGCAGCAGCAAGCACAAATACCCTCAGGGAGTTGGCCTCACAGGCAACACCTGAC 801 ACAACAGGTGAAGCAGCAGCAAACAAATACCCTCAGGGAGTGGCCTCACAGGCAACACCTGAC 802 TGTGAGGCTCCCACAGGCACCAGGAAATACACCTCAGGGAGTGGCCTTCCAACACCTGAC 803 TGTGAGGCTCCCACAGGCACCAGCAAAACACCAAACACCATTCCAACACCTGAC 804 TGTGAGGCTCCCAACACCAAGCCAGCCAGCCAGCCAGTTGGGGAGCCAAACCCAAACACCCATCTGAGAATTG 805 ACAACTGTGGGAAGCCAACCCAGCCAGCCAGCCAGCCAGTTGGGGAACCCAAACCCAAACACCCATCTGAGAATTG 807 AGAATTGAGGCCAAACCCAAACACCAAACACCATCTGAGAATTG 808 TACAACTCTGCGGAGGCGCAGCCAGCCAGCCAGGACCCAAACCCAAACACCCATCTGAGAACTG 809 ACAACTCTGCGGAGGCGCAGCCAGCCAGCCAGGCCCAGGCCCCCAAACCCAAACACCCACCCAGGGCCCCCAGGG 809 ACAACTCTGCGGAGGCCACCAAACCCAAAACACCCAACGACCAACTG 809 ACAACTCTGCGGAGGCGCCAGGCACCCAGGACCCCAAACCCCAAGCCCAACGCCCAACTG 809 ACAACTCTGCGGAAGGCCACCAGGCACCCAAACCCAAACACCCCAAGGGCCCCCC
677 ACHACHGETGHANGCAGGHAGCAGHATACCCTCAGGGHAGTGGCCTCACAGCGCAA 1736	677 ACAACAGGTGAAGCAGCAAGAATACCCTCAGGGAGTTGGCCTACAGGCAAGCAA
677 ACHACHGETGANGCAGCAGGAGCHGHATHACCCTCAGGGAGTGGCCTCACAGCGCAGCAA 1736	677 ACAACAGGTGAAGCAGCAAGAATACCCTCAGGGAGTTGGCCTACAGCGCAACT 1786 801 ACAACAGGTGAAGCAGCAGCAAGCAAATACCCTCAGGGAGTTGGCCTCACAGGCAACT 1786 801 ACAACAGGTGAAGCACCAGGAAATACCCTCAGGGAGTTGGCCTCACAGGCAACACCTGAC 1786 801 ACAACAGGTGCCCACAGGCACCAGCAAACCAAAACAACAGGATTGGCCTTCCAACACCTGAC 1796 91
677 ACHACHGETGANGCAGCAGGAGCHGHATHACCTTCAGGGAGTGGCCTCACCACGCACCACCACCACCACCACCACCACCACCACCAC	677 ACAACAGGTGAAGCAGCAAGAATACCCTCAGGGAGTTGGCCTACAGGGAAT 1736 801 ACAACAGGTGAAGCAGCAGCAGAATACCCTCAGGGAGTTGGCCTACAGGGAAGCAA 1736 801 ACAACAGGTGAAGCAGCAGCAGCAAATACCCTCAGGGAGTTGACCCTCACAGGCAGCAA 1866 737 GTGAGGCTCCCACAGGCACCAGCAAAACAACAACAGAATGAAT
677 ACAACAGGTGAAGCAGGAGCAGAATTACCCTCAGGGAGTGGCCTCACAGCGCAGCAA 1736	677 ACAACAGGTGAAGCAGCAAGAATACCCTCAGGGAGTTGGCCTACAGGCAGCAA 1736 801 ACAACAGGTGAAGCAGCAGCAGAATACCCTCAGGGAGTTGGCCTCACAGGCAGCAA 1736 801 ACAACAGGTGAAGCAGCAGCAGCAAATACCCTCAGGGAGTTGGCCTCACAGGCAGCAA 1860 737 GTGAGGCTCCCACAGGCACCAGCAAAACAACAACAGATGAATGTAGCCCTTCCAACACCTGAC 1736 861 GTGAGGCTCCCACAGGCACCAGCAAACACACAGGAATGAAT
677 ACAACAGGTGAAGCAGGAGCAGAATTACCCTCAGGGAGTGGCCTCACAGCACACCAA 1736	677 ACAACAGGTGAAGCAGCAAGAATACCCTCAGGGAGTTGGCCTACAGGGAATTACTTTTTAGC 801 ACAACAGGTGAAGCAGCAGCAAATTACCTTCAGAGGAATTACCAAAGCCCAAGCAAATTACCAAAGCACCAGGAATTACCTTCAGAGGCACCAGCAAATTACCAAAACCAGGAAATTACCTTGAGGATTGACCCTTCCAACACCTGAC 196 [
677 ACAACAGGTGAAGCAGGAGCAGAATTACCCTCAGGGAGTGGCCTCACAGCCACCAACACCAATTACTTGAAACACCATTTTTTTT	677 ACAACAGGTGAAGCAGCAAGAATACCCTCAGGGAGTTGGCCTACAGGGCAA 1736 801 ACAACAGGTGAAGCAGCAGCAAGAATACCCTCAGAGGAGTTGGCCTCACAGGCAGCAA 1736 801 ACAACAGGTGAAGCAGCAGGAAATACCCTCAGGGAGTGGCCTCACAGGCAGCAA 1866 707 GTGAGGCTCCCACAGGCACCAGCAAAATACCCTCAGGGATTGAGCCTTCCAACACCTGAC 1796 81 GTGAGGCTCCCACAGGCACCAGCAAAACACACGGATGAATGTAGCCCTTCCAACACCTGAC 1797 81 AGAATGAGACCAAACGCAGCCAGCCAGCAAATACACCAGAAACCCAAAACCCAAGCCATCTGAGGAATG 1856 857 AGAATGAGACCAAACGCAGCCAGCCAGCCAGCCAGTTTGGCAGAACCCAAAACCCAAGCCATCTGAGGAATG 1867 857 AGAATGAGACCAAACGCAAGCCAGCCAGGACTCTGGCGAGACCCAGAAACCCAAGCCCAGGGACTG 857 AGAATGTAGGACCAAACGCAGCCAGGCACTCTGCCAGAACCCAAACCCCAGGGGCCCGCCC
677 ACHACAGGTGHAGCAGGAGCAGAHATACCCTCAGGGAGCTGGCCTCACAGCGCACA 1736	677 ACAACAGGTGAAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTACAGGGCAA 1736 801 ACAACAGGTGAAGCAGCAGCAAATACCCTCAGAGGAAGTTGGCCTCACAGGCAGCAA 1736 801 ACAACAGGTGAAGCAGCAGGAAATACCCTCAGGGAGTGGCCTCACAGGCAGCAA 1866 807 GTGAGGCTCCCACAGGCACCAGGAAATACCCTCAGGGAGTGACCCTCACAGGCCAGCAA 1866 808 GTGAGGCTCCCACAGGCACCAGCAAAATACCCTCAGGGAGTGAATGTAGCCTTCCAACACCTGAC 1796 809 GTGAGGCTCCCACAGGCAACCCAGCCAAATACACCGAATGAAT
677 ACHACAGGTGHAGCAGGHAGCAGHATHACCTTCAGGGHATTGACTCACAGCACACAAATTACCTTCAGGGHATTGACTCACAGCACACAAATTACCTTCAGGGHATTGAGCACACACACACACAAATTACCTTCAGGGHATTGAGCCTTCACAGCCAACACCAGCAAATTACCTCAGGGHATTGAGCCTTCCACAGCCAACACCTGACACAGCAAATTACCCTCAGGGHATTGAGCCTTCCACAGCCAGCCAACACCAGCAAATTACCCTCAGGGATGAATTGAGCCTTCCAACACCCTGACACTGACACTGACACCTGACACTGACACACCTGACACACCTGACACACCTGACACACCTGACACACCTGACACACAC	677 ACAACAGGTGAAGCAGCAAGAATACCCTCAGGGAGTTGGCCTACAGGCAGA 1736 801 ACAACAGGTGAAGCAGCAGCAAATACCCTCAGGGAGTTGGCCTCACAGGCAGCAA 1736 801 ACAACAGGTGAAGCAGCAGCAAATACCCTCAGGGAGTGGCCTCACAGGCAGCAA 1866 801 ACAACAGGTGAAGCAGCAGGAAATACCCTCAGGGAGTGGCCTCACAGGCAGCAA 1866 802 TGGAGGCTCCCACAGGCACCAGGAAATACCCTCAGGGAGTGGACCTTACAGCCAACCTGAC 1796 803 TGGAGGCTCCCACAGGCAACCGCAGCAAATACACCAAAATTCAGCCAAACCCTGACAATG 1866 804 ACAACAGCTGCAAACGCAGCCAGCCAGATCGGGAGGCAAACCCAAACACCTGACATG 1867 907 AGAATGAGGCCAAACGCAGCCAGCCAGATCGGGAGGCCAAACCCAAACACCCATCCAAGCAATG 1868 908 ACAAACTCTGCGGAGGCGCAGCCAGCAATCGGCCCCGAGGCCCTGAGAACCCCAGGGCCCCCAGGGACTCTGCCCAGGGCCCCCAGGGCCCCCCAGGACTCTGCCCAGGCCCCCCCC
677 ACHACHGETGHANGCAGGHAGCHANATRACCTTCAGGHAGTGGCCTCACCACGCACA 1736	677 ACAACAGGTGAAGCAGCAAGACAAATACCCTCAGGGAGTTGGCCTACAGGGCAA 1736 801 ACAACAGGTGAAGCAGCAGCAAACACAAATACCCTCAGGGAGTTGGCCTCACAGGCAACACTACTAGAACACCAACACCTGACCAAAACACCAAAATACACCTCACAGGAAATACACCTCAGGAAATACACCTCACAGGAAATACACCTCACAGGAAATACACCTCACAGGAAATACACCTCACAGGCACCAACCA
677 ACHACHGETGHANGCHGHAGCHANATHACCTICAGGGAGTGGCCTCACCHCACGCACA 1736	677 ACAACAGGTGAAGCAGCAAGAATACCCTCAGGGAGTTGGCCTCACAGGCAAAT 1736 801 ACAACAGGTGAAGCAGCAGCAAATACCCTCAGGGAGTTGGCCTCACAGGCAAAT 1860 801 ACAACAGGTGAAGCAGCAGGAAATACCCTCAGGGAGTCGCCTCACAGGCAACACCTGAC 1860 801 ACAACAGGTGAAGCAGCAGGAAAATACCCTCAGGGAGTCGCCTCACAGGCAGCAA 1860 801 ACAACAGGTGAAACCAAGCAAAATACCCACAGGAATTGAGCCTTCCAACACCTGAC 1790 11111111111111111111111111111111111
677 ACHACHGETGHANGCHGHAGCHANATHACCTICAGGGHATTGACTCACHCACCCACHACACACCACA 1736	677 ACAACAGGTGAAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTCACAGGCAAT 1736 801 ACAACAGGTGAAGCAGCAGCAAATACCACTCACAGGGAGTTGGCCTCACAGGCAACAATACACCTGACAGGAAATACACCTGACAGGAAATACACCTGACAGGAAATACACCTGACGAGGAATACACCTGACCTGACAGGAAATACACCTGACAGGAAATACACCTGACCTGACAAGCCAACCTGACACCTGACTGA
677 ACHACHGETGHANGCHGHAGCHAHATHACCTICAGGGHAGTGGCCTCACHCGCCACHA 1736	677 ACAACAGGTGAAGCAGCAAGAAATACCCCTCAGGGAGTTGGCCTACACGCCACAAATACTTTTTTTT
677 ACHACHGETGHANGCHGHAGCHANATHACCTTCAGGAHCTGACCTCACAGGCAA 1736	677 ACAACAGGTGAAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTACAGGGCAA 1736 801 ACAACAGGTGAAGCAGCAGCAAAATACCCTCAGGGAGTTGGCCTCACAGGCAACAAATACCACTGACTAGAAATACCACTGACAGGAAATACCACTGACAGGAAATACACCTGACAAAATACACCTGACAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAACACCAAAAATACACCAAAAATACACCAAAAACAAC
677 ACHACHGETGHANGCHGHAGCHAHATRACCTTCAGGAHCTGACCTCACAGGCAA 1736	677 ACAACAGGTGAAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTACAGGGCAA 1736 801 ACAACAGGTGAAGCAGCAGCAAAATACCACTCAGGGAGTTGGCCTCACAGGCAACAAATACCACTCAGGGAGTTGACCCTCACAGGCAACACCTGAC 1860 801 ACAACAGGTGAAGCAGCAACACAGAAATACCACTGAGTAATTTAGCCCTTCCAACACCTGACAACACCTGAC 1860 801 ACAACAGGTGAAGCACAGGCACCAAGAAATACCACTGAGTAATTTAGCCCTTCCAACACCTGAC 1797 1111111111111111111111111111111111
677 ACHACHGETGHANGEAGHAGEAGHATACCCTCAGGGAGTGGCCTCACAGCGCAGCAA 1736	677 ACAACAGATGAAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTACAGCGCAA 1736 801 ACAACAGATGAAGCAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTCACAGCGCAA 1736 801 ACAACAGGTGAAGCAGCAAGAAATACCACTCAGGGAGTCGCCTCACAGCGCAACACCTGAC 801 ACAACAGGTGAAGCACCAGGCAAAACAAAATACCCCTCAGGGAGTCGCCTCCACAGCGCAGCAA 1866 801 ACAACAGGTGAAGCACCAGGCACCAGCAAAACAAAATACCCCTGAGAATCGAGAATTGAGCCCTTCCAACACCTGAC 1797 ACAATTGAGGCCCAACCCAGCCAGCAAAACAAAACACCAAAACCAAAACACCATCGAATTGAGCCCTTCCAACACCTGAC 1898 AGAAGTCTGCGAAGGCACCAGCCAGCCAGGACCCAGCCAG
677 ACHACHGETGHANGEAGHAGHAGHATANCCTTCAGGAHTGACTCACACCACACCACA 1736	677 ACAACAGGTGAAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTACAGGGCAA 1736 801 ACAACAGGTGAAGCAGCAGCAAATACCACTCAGGGAGTTGGCCTCACAGGCAACAATACCAACAGGAAATACACCTCAGGGAGTTGGCCTCACAGGCAACACCTGACTAAATACACCTCAGGAATTGAGCCCTTCCAACACCTGACTAAATACACCTGACTAAATACACCTCAGGAATTGAGCCCTTCCAACACCTGACTAAATACACCTGACTAAATACACCTGACAAAACAACACCTGACTAAATACACCTGACTAAATACACCTGACCAAAACAACACCTGACTAAATACACCTGACAAAACAACACCTGACTGA
677 ACHACHGETGHANGEAGHAGHAGHATANCCTTCAGGAHTGACTCACACCACACCACA 1736	677 ACAACAGGTGAAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTACAGGGCAA 1736 801 ACAACAGGTGAAGCAGCAGCAAATACCACTCAGGGAGTTGGCCTCACAGGCAACAATACCAACAGGAAATACACCTCAGGGAGTTGGCCTCACAGGCAACACCTGACTAAATACACCTCAGGAATTGAGCCCTTCCAACACCTGACTAAATACACCTGACTAAATACACCTCAGGAATTGAGCCCTTCCAACACCTGACTAAATACACCTGACTAAATACACCTGACAAAACAACACCTGACTAAATACACCTGACTAAATACACCTGACCAAAACAACACCTGACTAAATACACCTGACAAAACAACACCTGACTGA
677 ACHACHGETGHANGEAGHAGHACHATHACCTICAGGAATTGACCTACACGCACACCACACCACACACACACA	677 ACAACAGGTGAAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTACAGGGCAA 1736 801 ACACAGGTGAAGCAGCAGCAGAAATACCCTCAGGGAGTTGGCCTCACAGGCAACAATACCAACAGGTGAACCAAGGAAAATACCACTCAGGGAGTTGGCCTCACAGGCAACACCTGACTAAATACACCAGGAAATTGTAGCCCTTCCAACACCTGACTAAATACAACAACACCTGACTAAATACAACAACACCTGACTAAATACAACAACACCTGACTAAATACAACAACACCAAAACAACACCTGACTAAAACAACAACACCAAAACAACACCAAAACAACACCTGACTAAATACAACAACACCAAAACAACACCAAAACAACACCTGACTAAACACCAAAACAACACCAAAACAACACCTGACTAGGAACCAAAACCAAAACACCAACACCTGACTAGGAATTGTAGAACCAAAACCAAAACACCAACACCTGACTAGGAATTGTAGAACCAAAACCAAAACCAAAACCAAAACACCTGACTAGGAATTGTAGAACCAAAACCAAAACCAAAACCAAAACCAAAACCAAAACCAAAA
677 ACHACHGETGHANGEAGHAGHAGHATANCCTTCAGGAHTGACTCACACCACACCACA 1736	677 ACAACAGGTGAAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTACAGGGCAA 1736 801 ACAACAGGTGAAGCAGCAGCAAATACCACTCAGGGAGTTGGCCTCACAGGCAACAATACCAACAGGAAATACACCTCAGGGAGTTGGCCTCACAGGCAACACCTGACTAAATACACCTCAGGAATTGAGCCCTTCCAACACCTGACTAAATACACCTGACTAAATACACCTCAGGAATTGAGCCCTTCCAACACCTGACTAAATACACCTGACTAAATACACCTGACAAAACAACACCTGACTAAATACACCTGACTAAATACACCTGACCAAAACAACACCTGACTAAATACACCTGACAAAACAACACCTGACTGA
677 ACHACHGETGHANGEAGHAGEAGHATACCCTCAGGGAGTGGCCTCACAGCGCAGCAA 1736	677 ACAACAGATGAAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTACAGCGCAA 1736 801 ACAACAGATGAAGCAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTCACAGCGCAA 1736 801 ACAACAGGTGAAGCAGCAAGAAATACCACTCAGGGAGTCGCCTCACAGCGCAACACCTGAC 801 ACAACAGGTGAAGCACCAGGCAAAACAAAATACCCCTCAGGGAGTCGCCTCCACAGCGCAGCAA 1866 801 ACAACAGGTGAAGCACCAGGCACCAGCAAAACAAAATACCCCTGAGAATCGAGAATTGAGCCCTTCCAACACCTGAC 1797 ACAATTGAGGCCCAACCCAGCCAGCAAAACAAAACACCAAAACCAAAACACCATCGAATTGAGCCCTTCCAACACCTGAC 1898 AGAAGTCTGCGAAGGCACCAGCCAGCCAGGACCCAGCCAG
677 ACHACHGETGHANGEAGHAGEAGHATACCCTCAGGGAGTGGCCTCACAGCGCAGCAA 1736	677 ACAACAGGTGAAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTACAGGGCAA 1736 801 ACAACAGGTGAAGCAGCAGCAAAATACCCTCAGGGAGTTGGCCTCACAGGCAACAA 1860 801 ACAACAGGTGAAGCAGCAAGAAATACCACTCAGGGAGTCGCCTCACAGGCAACACCTGAC 801 ACAACAGGTGAAGCACCAGGAAAACAAAATACCCCTCAGGGAGTCGCCTCACAGGCACACCTGAC 801 TGAAGGCTCCCACAGGCACCAGCAAAACAACACCAAAACCAAAGCCAACACCTGAC 802 TGAAGGCTCCCACAAGGCAACCAACCAACACCAACACCTGAC 803 ACAACTGGAGGCGCCAGCCAGCCAGGACCAACCAAAACCAAAACCAAAACCACC
677 ACHACHGETGHANGEAGHAGEAGHATACCCTCAGGGAGTGGCCTCACAGCGCAGCAA 1736	677 ACAACAGATGAAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTACAGCGCAA 1736 801 ACAACAGATGAAGCAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTCACAGCGCAA 1736 801 ACAACAGGTGAAGCAGCAAGAAATACCACTCAGGGAGTCGCCTCACAGCGCAACACCTGAC 801 ACAACAGGTGAAGCACCAGGCAAAACAAAATACCCCTCAGGGAGTCGCCTCCACAGCGCAGCAA 1866 801 ACAACAGGTGAAGCACCAGGCACCAGCAAAACAAAATACCCCTGAGAATCGAGAATTGAGCCCTTCCAACACCTGAC 1797 ACAATTGAGGCCCAACCCAGCCAGCAAAACAAAACACCAAAACCAAAACACCATCGAATTGAGCCCTTCCAACACCTGAC 1898 AGAAGTCTGCGAAGGCACCAGCCAGCCAGGACCCAGCCAG
677 ACHACHGETGHANGEAGHAGEAGHATACCCTCAGGGAGTGGCCTCACAGCGCAGCAA 1736	677 ACAACAGATGAAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTACAGCGCAA 1736 801 ACAACAGATGAAGCAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTCACAGCGCAA 1736 801 ACAACAGGTGAAGCAGCAAGAAATACCACTCAGGGAGTCGCCTCACAGCGCAACACCTGAC 801 ACAACAGGTGAAGCACCAGGCAAAACAAAATACCCCTCAGGGAGTCGCCTCCACAGCGCAGCAA 1866 801 ACAACAGGTGAAGCACCAGGCACCAGCAAAACAAAATACCCCTGAGAATCGAGAATTGAGCCCTTCCAACACCTGAC 1797 ACAATTGAGGCCCAACCCAGCCAGCAAAACAAAACACCAAAACCAAAACACCATCGAATTGAGCCCTTCCAACACCTGAC 1898 AGAAGTCTGCGAAGGCACCAGCCAGCCAGGACCCAGCCAG
677 ACHACHGETGHANGEAGHAGEAGHATACCCTCAGGGAGTGGCCTCACAGCGCAGCAA 1736	677 ACAACAGATGAAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTACAGCGCAA 1736 801 ACAACAGATGAAGCAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTCACAGCGCAA 1736 801 ACAACAGGTGAAGCAGCAAGAAATACCACTCAGGGAGTCGCCTCACAGCGCAACACCTGAC 801 ACAACAGGTGAAGCACCAGGCAAAACAAAATACCCCTCAGGGAGTCGCCTCCACAGCGCAGCAA 1866 801 ACAACAGGTGAAGCACCAGGCACCAGCAAAACAAAATACCCCTGAGAATCGAGAATTGAGCCCTTCCAACACCTGAC 1797 ACAATTGAGGCCCAACCCAGCCAGCAAAACAAAACACCAAAACCAAAACACCATCGAATTGAGCCCTTCCAACACCTGAC 1898 AGAAGTCTGCGAAGGCACCAGCCAGCCAGGACCCAGCCAG
677 ACHACHGETGHANGEAGHAGEAGHATACCCTCAGGGAGTGGCCTCACAGCGCAGCAA 1736	677 ACAACAGATGAAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTACAGCGCAA 1736 801 ACAACAGATGAAGCAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTCACAGCGCAA 1736 801 ACAACAGGTGAAGCAGCAAGAAATACCACTCAGGGAGTCGCCTCACAGCGCAACACCTGAC 801 ACAACAGGTGAAGCACCAGGCAAAACAAAATACCCCTCAGGGAGTCGCCTCCACAGCGCAGCAA 1866 801 ACAACAGGTGAAGCACCAGGCACCAGCAAAACAAAATACCCCTGAGAATCGAGAATTGAGCCCTTCCAACACCTGAC 1797 ACAATTGAGGCCCAACCCAGCCAGCAAAACAAAACACCAAAACCAAAACACCATCGAATTGAGCCCTTCCAACACCTGAC 1898 AGAAGTCTGCGAAGGCACCAGCCAGCCAGGACCCAGCCAG
677 ACHACHGETGHANGEAGHAGEAGHATACCCTCAGGGAGTGGCCTCACAGCGCAGCAA 1736	677 ACAACAGGTGAAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTACAGGGCAA 1736 801 ACAACAGGTGAAGCAGCAGCAAAATACCCTCAGGGAGTTGGCCTCACAGGCAACAA 1860 801 ACAACAGGTGAAGCAGCAAGAAATACCACTCAGGGAGTCGCCTCACAGGCAACACCTGAC 801 ACAACAGGTGAAGCACCAGGAAAACAAAATACCCCTCAGGGAGTCGCCTCACAGGCACACCTGAC 801 TGAAGGCTCCCACAGGCACCAGCAAAACAACACCAAAACCAAAGCCAACACCTGAC 802 TGAAGGCTCCCACAAGGCAACCAACCAACACCAACACCTGAC 803 ACAACTGGAGGCGCCAGCCAGCCAGGACCAACCAAAACCAAAACCAAAACCACC
677 ACHACHGETGHANGCHGHAGCHAHATRACCTTCAGGAHCTGACCTCACAGGCAA 1736	677 ACAACAGGTGAAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTACAGGGCAA 1736 801 ACAACAGGTGAAGCAGCAGCAAAATACCACTCAGGGAGTTGGCCTCACAGGCAACAAATACCACTCAGGGAGTTGACCCTCACAGGCAACACCTGAC 1860 801 ACAACAGGTGAAGCAGCAACACAGAAATACCACTGAGTAATTTAGCCCTTCCAACACCTGACAACACCTGAC 1860 801 ACAACAGGTGAAGCACAGGCACCAAGAAATACCACTGAGTAATTTAGCCCTTCCAACACCTGAC 1797 1111111111111111111111111111111111
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677 ACHACHGETGHANGCHGHAGCHANATHACCTTCAGGAPTGGCCTCACHCGCCACHACT 1736	677 ACAACAGGTGAAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTACACGCCAGAATTACTTTAAGAAATTACTTTTAGGCAAATTACTTTAAGAATAATATATAT
677 ACHACHGETGHANGCHGHAGCHANATHACCTICAGGANCTGGCCTCACAGGCACA 1736	677 ACAACAGGTGAAGCAGCAAGAAATACCCTCAGGGAGTTGGCCTACAGGGCAA 1736 801 ACAACAGGTGAAGCAGCAGCAAATACCCTCAGGGAGTTGGCCTCACAGGCAACACTAGACTAGAATACACCAAAAATACACCAAAATACACCAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAAATACACCAAAATACACCAAAATACACCAAAATACAACCAAAATACACCAAAATACACCAAAATACACCAAAATACACCAAAATACACCAAAATACACCAAAATACACCAAAATACACCAAAATACAACCAAAAATACACCAAAATACAACCAAAAATACACCAAAAATACAACCAAAAATACAACCAAAAAA
677 ACHACHGETGHANGCHGHAGCHANATHACCTICAGGGAGTGGCCTCACCHCACGCACA 1736	677 ACAACAGGTGAAGCAGCAAGAATACCCTCAGGGAGTTGGCCTCACAGGCAAAT 1736 801 ACAACAGGTGAAGCAGCAGCAAATACCCTCAGGGAGTTGGCCTCACAGGCAAAT 1860 801 ACAACAGGTGAAGCAGCAGGAAATACCCTCAGGGAGTCGCCTCACAGGCAACACCTGAC 1860 801 ACAACAGGTGAAGCAGCAGGAAAATACCCTCAGGGAGTCGCCTCACAGGCAGCAA 1860 801 ACAACAGGTGAAACCAAGCAAAATACCCACAGGAATTGAGCCTTCCAACACCTGAC 1790 11111111111111111111111111111111111
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RESULT 9
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SOURCE
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REFERENCE AUTHORS

ACO20629 142971 bp DNA linear PRI 07-MAR-2002 Homo sapiens 12g BAC RP11-76E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence. AC020629 AC020629.6 GI:7656675

ISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Craniata; Craniata; J., Blankenburg; K.,

Bunac, C.,

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Yang, A.M., Yang, R., Yu, W., Zhou, X., Kucherlapati, R., Melson Xhang,A.M., Yang,R., Yu,W., Zhou,X.,
Gibbs,R.
Direct Submission

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Submitted (28-APR-2000) Human Genome Sequencing Center, Depar of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
[bases 1 to 142971)
Submitted (07-MAR-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Apr 27, 2000 this sequence version replaced gi:7025656. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
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Overlapping clones are noted at the beginning and end of the Features listing. CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are c sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. only

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found

http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

QUALSTAT-REPORT

Number of N's in consensus :	Number of consensus changing edits:	Fraction of Phrap values less than 40 :	Average error rate (BCM-Phrap estimate):	Phrap values in estimate:	Contig length:	Summary Statistics
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RP11-325P15 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBace3.6

Group. Further information can http://www.sanger.ac.uk/HGP/Chrl

Further information can be

found at

http://www.sanger.ac.uk/Projects/C elegans/wormpep This seq was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1

sequence 1 Mapping

database can be found at

assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP

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                                                                                                  Submitted (08-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 11, 2001 this sequence version replaced gi:15022347.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with This sequence was finished as follow.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the
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Mammalia; Eutheria;
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Primates;
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                                                               GCGGATCCTGGTCCCCACC-----CAGTTTGTTGGTGCCATCATCGGAAAGGAGGCCTT
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                             GACCATAAAGAACATCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAA
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/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RPP11-35EP15"
/clone_lib="RPCI-11.2"
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 11 AC015706 LOCUS DEFINITION 182695 bp DNA linear HTG 24-AUG-2002 SEQUENCE, 17 unordered pieces.
AC015706 AC01570 HTG; HTGS_PHASE1; HTGS_DRAFT.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 182695)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 1, clone RP11-325P15 Homo sapiens (human)

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS Unpublished

TITLE JOURNAL

REFERENCE AUTHORS

O'RE STREET TO 182695)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Barren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Barren, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cocke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, M., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McBarnan, R., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., McKernan, K., McLaughlin, J., Meldrim, J., McKernan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, M., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Direct Submission

BL Research, 320 Charles Street, Cambridge, MA 02141, USA

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Bactien, V., Beda, F., Boguslavkiy, L., Boukigalter, B., Brown, A., Burkett, G., Bardavkiy, L., Boukigalter, B., Brown, A., Burkett, G., Collymore, A., Coske, F., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fizhugh, M., Gage, D., Grand, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Lin, G., Locke, K., Macdonald, P., Marquis, N.,

COMMENT JOURNAL

Center code: WIBR Web site: http://v Center: Whitehead Direct Submission

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McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N., O'Neil,D., Olivar,T.M., Raymond,C., Riley,R., Rogov,P., Rothman,D., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Doy, A. Canton D. Cohange C. Consor, D. Consor, D. Cohange C. Consor, D. Consor, D. Consor, D. Cohange C. Consor, D. Co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 26, 2000 this sequence version replaced gi:6454072. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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117051: gap of 100 bp
143611: contig of 26560 bp
143711: gap of 100 bp
182695: contig of 38984 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                84.7%;
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           0
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32809 32909 37001 37101 45184 45284 53422 53422 53522 64477 64577

18481 18581 23094 23194 28214 28314

23093:

18580 18480

32908: 37000:

120 19365

19425

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6170 10461 10561 14301 14401

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	241 CTCTCG
CTCTGGAGCTGCAGATTICTTGAAAAATTCCTCTGAAAATTCCTCTGAAAAATTTGAAGAAATTTGAAGAAATTTGAAGATTTGAAGATTTGAAGATTTGAAGAA	CTCTCGGGTAAAA AGCTTAAGAGGC AAGCTTAAGAAGCT TTGGATGGACTT TTGGATGGACTT TTGGATGGACTT GACACAGAAACCT GATGAAGAGGTAA
AGAGAAGCCT	PIGGAATTG
AGAAGCCTGTCACCAT	ATGGGAAAA ATGGGAAAAA ATGGGAAAAA ATGGGAACAG ATGGGACAG ATGGAACAG ATGGAACA
ATGCCACCCAG	CCCGGGTAGG Treggraca
CTCTGGAGCTGCAGAAAGCCTGTCACCATCCATGCACCCCAGAGGGGACTTCTGAAAGCTICCTGAAGCCTGCAGAGGGAACTTCTGAAGCCTICCTGAAGCCTGCAGAGAGCGAACTTCTGAAGCCTCTGAAGCATCCATC	CTCTCGGGTAAAGTGGAATTGCATGGGAAAATCATGGAAAGTTGATTACTCAGTCTTAAA
TCTGAAGC GCCGAAGA AAAGAAGG GCCTTTGCA TCTTTGCA TGATATGC TGATATCC	
830 20080 890 20140 950 201188 1010 20248 1109 20368 11129 20368 11129 20428 1189 20428 1189 20428	300 19545 360 19605 19605 19720 19720 19780 537 19780 597 199840 656 19980 19960
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RESULT 12 AC104980 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Qy 32 Db 225	Qу 32 Db 224	Qy 3160 Db 22399	Qy 3101 Db 22339	Qy 304 Db 2227	Qy 298 Db 2221	Qy 29: Db 221:	Qy 2863 Db 22102	Qy 280 Db 2204	Oy 2743 Db 21982	Qy 2683 Db 21922	Qy 2624 Db 21862	Qy 2564 Db 21802	Qy 2504 Db 21742	Qy 2444 Db 21682	Db 2162
ACI04980 ACI04980 Homo sapiens chromosome 8, clone RPI1-281D17, complete sequence. ACI04980 ACI04980.5 GI:19849375 HTG. HTG. HTG. sapiens (human) Homo sapiens (human)	3280 ATT 3283 2519 ATT 22522	220 TTGTCTTCCGCTAGCCAAGAACCNATATGGCCTTCTTTTGGACAAACCTTGAAAATGTTT 3279 	60 AAGATATCAACTGCCAGCCTGGAGAAGGTGACAGTCCAAGTGTGCAACAGCTGTTCTGAA 3219 		2 GCTACCTCAGGTG-TITITACCTCAGCA	82 GTTGTTGGCCCAGGGCGTTAAATTCACAGATTTTTTAACGAGAAAAACACACAGAAAAAA 3041 		63 TCCACAATGAAAGAAIGTATITTGTC-TTTTIGCATITTGGIGTATAAGCCATCAATATT 2921 02 TCCACAATGAAAGAAGGTGTTTTGTCTTTTTTGCATITTGGIGTATAAGCCATCAATATT 22161	803 TTTTGGAAGAGAAAACAGGAACCCACCAAACCAATCAACCAAACAAA	43 CAGCCTCAACTTACACTTGGTTACTCAAAAGAACAAGAGTCAATGGTACTTGTCCTAGCG 2802 	33 GGCAAAGCAGTGCTCTGAGTATCACATCACACAAAAGGAACAAAAGCGAAACACACAC	24 CTTTTGAATTTCCTCATCCCCATCTCAATCCCGTATCTACGCACC-CCCCCCCCCC	64 CTCTGTCTCTCTGTTTATCTCTCCCCTCCCTCCCCTCTCTCT	04 CACCCATTCTCTTIGCTTCACAGGITTTAAACIGGITTTITGCAIACIGCTAIAIAATI 2563 	4 AAGGGATACCGTCTCCTTGAAGAAGGAAACTCTGTCACTCCTCATGCCTGTCTAGCTCATA 2503 	
		RE						REI	5.11					hed.	REST I	REF

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AUTHORS
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Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Jones, C., Kamat, A., Kartas, A., Kells, C., LaRocque, K.,
Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,
MacChaen, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
McCarthy, M., McEwan, P., McKernan, K., Pierre, N., Pollara, V.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Es 3 (bases 1 to 187226)

Es 3 (bases 1 to 187226)

Es 3 (bases 1 to 187226)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Chazaro, B., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Faros, S., Ferreira, F., Kells, C., Lakcoque, K., Limazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Kells, C., Lakcoque, K., Lamazares, R., Landers, T., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., McCarthy, M., McEwan, P., McEwran, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Morbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Oliver, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Schage-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ve, W.J., Young, G., Limer, A. and Zody, M.

Direct Submission

Mircett Submission

Mattheward Toerter for Genome
RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Kanatas, A., Kells, C., LaRocque, K., Lamazares, R., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Morbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 8, clone RP11-281D17
Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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4 (bases 1 to 187226)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Riback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (31-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 31, 2002 this sequence version replaced gi:19683374. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
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Center clone name: 281_D_17
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complement (22312. .24467)

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REFERENCE
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RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Schaefer, C.M., Schuler, G.D.,

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Generation and initial analysis of more than 15,000 full-length
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IMAGE:5354659), partial cds.
BC023758
Contact: nisc_mgc@nhgri.nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

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McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                              Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                USA
NIH-MGC Project URL: http://mgc.nci.nih
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (05-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene Collection (MGC), Cance Institute, 31 Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                     Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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                    AAGAACATCACTAAGCAGACCCAGTCCCGGGTAGACATCCACAGAAAGGAGAACTCTGGG
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through the I.M.A.G.E. Consortium/hum an hope, series: IRAK Plate: 55 Row: 0 Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction.
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/lab_host="DH10B"
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ACAG 17	Db 1622 AACTTAACCAGAGGTCATCGTGCTCGTGACCAGACGCCAGATGAAAATGAGGAA 1608 1622 AACTTGACAAGTTCATCGTGCTCGTGACCAGACGCCAGATGAAAATGAGGAA 1608 1622 AACTTGACAAGTGCAGAAGTTATCGTGCCTCGTGACCAAACGCCAGACGAGAAGATCAGG 1668 Qy 1609 GTGATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACGACAGAGCACAAGATCAGG 1668	1489 1562	4 D 4 D	1322 CAGGCTGTGGGTGCTATCATCGGGAAGGAGGGGGCACACATCAAACAGCTCGCTC		11	141141	1138		OY 958 TIGAAGAAAATGAACAAGAACAAGAACAAGATAACAATCTCATCTTTGCAGGATTTG 1017 DD 902 CIGAAGAAAAACATGAACAAGGACCAAGATAACAATCTCATCTTTGCAGGATTTG 1017 DD 902 CIGAAGAAAATAGAACATGAGAACAAGGACCAAGATAAACCATCTCATCCTTGCAGGATTTG 961 OY 1018 AGCATATACAACCCGGAAAGAACCATGTGTGAAGGACAAGTTGAAGGCCAGT 1077 OY 1018 AGCATATACAACCCGGAAAGAACCATGTGAAGGGCAAGTTGAAGGCCTGTGCCAGT 1077	898 CTGAAAATCTTGGCACACAATGGCTTGGTTGGAAGACTGATTGGAAAAGAAGGCAGAAAT	838 782	υ
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Nielsen,J., Christiansen,J., Lykke-Andersen,J., Johnsen,A.H., Wewer,U.M. and Nielsen,F.C.
A family of insulin-like growth factor II mRNA-binding proteins represses translation in late development Mol. Cell. Biol. 19 (2), 1262-1270 (1999)
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Nielsen,J., Christiansen,J., Lykke-Andersen,J., Johnsen,A.H.,

Wewer,U.M. and Nielsen,F.C.

Direct Submission
Submitted (30-DEC-1998) Institute of Molecular Biology, University
of Copenhagen, Soelvgade 83H, Copenhagen DK-1307, Denmark

Location/Qualifiers
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Homo sapiens IGF-II mRNA-binding
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/protein_id="AAD09827.1"
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1812 ACCCTC. 1766 ACGGATT 1872 ACGGATT 1826 CGGGAGT 1826 CGGGAG 1932 CGGGAG 1886 GCCGAGG 111111 1992 GCCGAGG
1812 ACCCTCAGGAGTCGCCTCACAGCGAGCAAGTGAGGCTCCCACAGGCACAAAACA 1871 1766 ACGGATGAATGTAGCCCTTCCAACACCTGACAGATGAGACCAAACGCAGCCAGC

Search completed: July 24, 2004, 13:04:44 Job time: 12667.7 secs

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Minimum DB
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13.1	15.4	15.6	16.0	16.0	17.8	18.3	18.6	19.6	20.9	21.1	21.1	21.1	21.2	21.2	21.2	21.2	21.2	21.2	21.2	21.2	21.2	2
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ALIGNMENTS

RESULT 1 AAZ36154 17-APR-1998; 16-MAR-1999; 28-OCT-1999. WO9954738-A1 Cancer associated An alternative AAZ36154 standard; DNA; 3283 BP (LUDW-) Homo sapiens 11-FEB-2000 AAZ36154; LUDWIG INST CANCER RES. (first 98US-00061709. 99WO-US005766 form of DNA encoding cancer associated antigen KOC-3. antigen; entry) KOC-3; cancer; vaccine; CT7;

WPI; 2000-013284/01. develop

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Nucleotides representing cancer-associated products for the diagnosis, monitoring and for the diagnosis, monitoring genes, used to develo

Claim 55; Page 42-43; 44pp; English.

The present sequence represents an alternative form of a cancer associated antigen gene designated KOC-3. The specification also describes a cancer associated antigen designated CT7. The CT7 polynucleotide was isolated from SK-MEL-37 melanoma cells. The polypeptide has some homology with MAGE-10, limited to about 210 carboxy terminal amino acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in serine, proline, plutamine and leucine, and an almost invariable core of the peptide given in AAY4387. The CT7 polypeptide can be processed to peptides which provoke lysis by cytolytic T cells. The polymucleotides and polypeptides can be used for treating a cancerous condition and screening for or diagnosing cancerous conditions. The cancer associated antigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or granulocyte

481 G 481 G 541 G 5601 G 6601 G 661 J 721 J 7721 J 7781 G 841 J 901 J	CC macrophage-colony stimulating factor (GM-CSF) XX sequence 3283 BP; 945 A; 833 C; 779 G; 725 T; 0 U; 1 Other; Query Match 100.0%; Pred. No. 0; Best Local Similarity 100.0%; Pred. No. 0; Marches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Marches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Marches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Marches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Marches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Marches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Marches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Marches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Marches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Marches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Marches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Marches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Marches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Marches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Marches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Marches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Marches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Marches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Marches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 120 Mis
	Db 961 AAGAAATTGAACCGGAAAGACCAACAGCCAAGATTTCAACCTTTTCAGGCCTTTCAGGCCTTTCAGGCCTTTCAGGCCTTTCAGGCCTTTCAGGCCTTTCAGGCCTTTCAGGCCTTTCAGGCCTTTCAGGCCCGAATTCCGGAATTCTCAGGCCGGAATTCTCAAACAGGTTGGCCCGGATTCCCGAATTCCCAAGCCCAGGCTTTCAGGCCCAATTCCAGGCTTTCAGGCCCGAATTCCGGAAACAGATTCTCAAACAGGTTGGCCCGGAATTCTCAGGCCTGTTCAGGCCTTTCAGGCCTTTCAGGCCTTTCAGGCCTTTCAGGCCAAACAGGTTGGCCCGAAACAGGTTGGCCCGAAACAGCTTCAGGCCTCTTTCAACAGATTGCCCAAACAGATTCGCCAAACAGATTCGCCAAACAGATTCGCCAAACAGATTCGCCAAACAGATTCGCCAAACAGATTCGCCAAACAGATTCGCCAAACAGATTCGCCAAACAGATTCGCCAAACAGATTCGCCAAACAGATTCGCCAAACAGATTCGCCAAACAGATTCGCCAAACAGATTCGCCAAACAGATTCGCCAAACAGATTCGCCAAACAGATTCGCCAAACAGATTCGAAAACAGATTCGAAAACAGATTCGAAAACAGATTCGAAAACAGATTCGAAAACAGATTCGAAAACAGATTCGAAAACAGATTCGAAAACAGATTCGAAAACAGATTCGAAAACAGATTCAACAGATTCAACAGTTCAACAGATTCAACAGATTCAACAGATTCAACAGATTCAACAGTTCAACAGATTCAACAGATTCAACAGATTCAACAGATTCAACAGATTCAACAGATTCAACAGTTCAACAGTTCAACAGTTCAACAGATTCAACAGATTCAACAGATTCAACAGATTCAACAGTTCAACAGTTCAACAGTTCAACAGTTCAACAGTTCAACAGTTCAACAGTTCAACAGTTCAACAGTTCAAACAGTTCAAACATTCAA

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2221 2221	ACTCCAATTTTAATCAATTATTAATTTTTTTTTTTT 228 ACTCCAATTTTTAATCAATTATTAATTTTTTTTTT
281 281	TTAGACTTTAAAGAATAAAGTCTTTGGGAGGTCTCACGG 234
41	ACCGGCACAAATTCACCCAGAGGGAAATCTCGTCGGA 2
40 40	AGGACACTCACGGCAGTTCTGGATCACCTGTGTATGTCAACAGAAGGGATACCGTCTCCT 2460
46	TGAAGAGGAAACTCTGTCACTCCTCATGCCTGTCTAGCTCATACACCCATTTCTCTTTGC 2520
2521 2521	TTCACAGGITTTAAACTGGITTTTTTGGATACTGCTATATAATTCTCTGTCTCTCTCTGTT 2580
2581 2581	TATCTCTCCCCTCCCTCCCCCTCCTCTTCTTCAATCTCCATCTTTGAATTTCCTCAT 2640
2641 2641	TATCTACGCACCCCCCCCCCCAGGCAAAGCAGTGCTC
2701 2701	GAAACACAAAACCAGCTCAACTTACACTT 276
2761 2761	<i>D</i> — <i>D</i>
2821 2821	GGAACCCAACCAACCAATCAACCAAACAAAGAAAAATTCCACAATGAAAGAATGT 2880
2881 2881	ATTITGTCITTTIGCATTITGGTGTATAAAGCCATCAATATTCAGCAAAATGATTCCTTTC 2940
2941 2941	TTGTTGGCCCAGGG
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	IGTAAAGCTGATAGTTGGAGCAT 31
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                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                    Claim 1; SEQ ID NO 6786; 103pp; English.
                                                                                                                                                                                                                                       biodiversity.
                                                                                                                                                                                                                                                                                    P-PSDB;
                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                             WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding novel human diagnostic protein #6786.
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                                                                                                                                                                                                                                                                                                              Liu C,
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                                                                                                                                                                                                                                                                                                              Tang YT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            forensic;
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and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also use in diagnostics as expressed sequence tags for identifying expressed The invention relates to isolated polynucleotide (I) and polypeptide (II) used

Sequence 3667 BP; 1081 A; 882 C; 846 G; 858 T; 0 U; 0 Other;

Query Match 99.1%; Score 3253.8; DВ ت. د

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A23 AGAAACCGCCGTTGTCAACGTCAATATGGGACAGTGGAAATGGGAAACAACCAAAATGACCAATGAAACACCCAAAATGGGACAATGGAAACACCCAAAATGACCAAAATGACCAAAATGACCAAAATGACCAATGAAAATGACCAATGAAAATGACCAATGAAAATGACCAATGAAAATGACCAATGAAAATGACCAATGAAAATGACCAATGAAAATAACCACCTAGAAATGACCAATGAAAATAACCACCAATGAAATGACCAATGAAAATAACCACCATGAAATGACCAATGAAATAACCACCATGAAAATAACCACCATGAAATGACCAATGAAATAACCACCATGAAATAACCACCATGAAATAACCACCAACAAAATAACCACCAAGAATTACCAATGAAATAACCACTAGAATTACCAATGAAATAACCACTAGAATTACCAATGAAAATAACCACATGAAATAACCACATGAAAATAACCACATGAAAATAACCACAATGAAATAACCAACC	3277 3277 3 3 3 6 63 - 63 - 123 123 183 183 183 183 183 183 183 183 183
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156 192 162 198 168 204 174 216 216 216 216 186 226 174 174 217 227 193 193 193 193 193 193 193 193 193 193	1389 ATACAACCCGGAAAGAACCATCACTGTGAAAGGGCACAGTTGAAGGCCTGTGCCAGTGCTGA 1448 1083 GATAGAGATTATGAAGAAGCTGCGTGAGGCCTTTGAAAATGATATGATGCTGGTGTAACAC 1142

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AGAAGGTGACAGTCCAAGTGTGCAACAGCTGTTCTGAATTGTCTTCCGCTAGCCAAGAAC
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viral meningitis;
lema; hydrocephalus;
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RE, JE, 듄 Gannavarapu M, Hoersch S, Kama Morrisey MP, Olandt PJ, Sen A, u K, Schmandt RE, Zhao X, Glatt Glatt K; Kamatkar S, Vieby PO, Kovatis S

(MILL-)

MILLENNIUM PHARM

P-PSDB; 2002-723277/78. ABG96346.

Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and from a non cancer patient.

Disclosure; Page 262-263; 481pp; English.

The present invention relates to a new method for assessing whether a CC patient is afflicted with ovarian cancer. The method involves comparing CC the expression level of a marker in a patient sample and the normal level CC of expression of the marker in a control non-ovarian cancer sample, where CC the marker is selected from 363 cancer markers described in the CC expecification. The method of the invention is useful in diagnosing or CC characterising cancer, in detecting the presence of cancer as early as CC possible, and the recurrence of ovarian cancer. The method may also be of CC particular use with patients having an enhanced risk of developing CC ovarian cancer (e.g. patients having a familial history of ovarian CC cancer). The cancer markers may be used in the management and treatment CC of e.g. brain and central nervous system discase), brain control of central meningitis, Alzheimer's disease or Parkinson's disease), brain disorders (e.g. bacterial or viral meningitis or encephalitis), testicular disorders (e.g. bacterial or viral meningitis or encephalitis), testicular disorders (e.g. nontuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be where level of.

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7 3	TAGAGAGGAGCTTTGAGGCCACCCGCACAAAATTCACCCAGAGGGAAATCTCGTCGGAAG 2402 	
7 4	GACACTCACGGCAGTTCTGGATCACCTGTGTATGTCAACAGAAGGGATACCGTCTCCTTG 2462 	
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                                                     The present sequence represents a cancer associated antigen gene designated KOC-3. The specification also describes a cancer associated antigen designated CT7. The CT7 polynucleotide was isolated from SK-MEL-37 melanoma cells. The polypeptide has some homology with MAGE-10, limited to about 210 carboxy terminal amino acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in serine, proline, glutamine and leucine, and an almost invariable core of the peptide given in AAY43877. The CT7 polypeptide can be processed to peptides which provoke lysis by cytolytic T cells. The polynucleotides and polypeptides can be used for treating a cancerous condition and screening for or diagnosing cancerous conditions. The cancer associated antigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony stimulating factor (GM-CSF)
     Sequence 3412 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 55; Page 41; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotides representing cancer-associated products for the diagnosis, monitoring and
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2000US-0234223P. 2000US-0234274P. 2000US-0234997P. 2000US-0234998P. 2000US-0235484P.

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The invention relates to isolated nucleic acid molecules and their concoded secreted proteins. The nucleic acids and proteins are used to grevent, treat or ameliorate a medical condition in e.g. humans, mice, crabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in calleviating symptoms associated with the disorders and in diagnostic diseases e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune considers e.g. rheumatoid arthritis, hyperproliferative disorders e.g. carrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to reguencate tissues and in chemotaxis. The polypeptides can also be used to and sound healing and epithelial cell proliferation, for supporting cell culture of primary tissues, to reguencate tissues and in chemotaxis. The polypeptides can also be used capabilities, fat content, lipid, protein, carbohydrate, vitamins, and equence encodes a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed
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Best Local Similarity
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P-PSDB; AAU16163.
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                 GGATGATGAACAAGCTTTACATCGGGAACCTGAGCCCCGCCGTCACCGCCGACGACGACCTCC
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                                        AAGAACCNATATGGCCTTCTTTTGGACAAACCTTGAAAATGTTTTATTT
                                                                                                                                                   GCCTGGAGAAGGTGACAGTCCAAGTGTGCAACAGCTGTTCTGAATTGTCTTCCGCTAGCC
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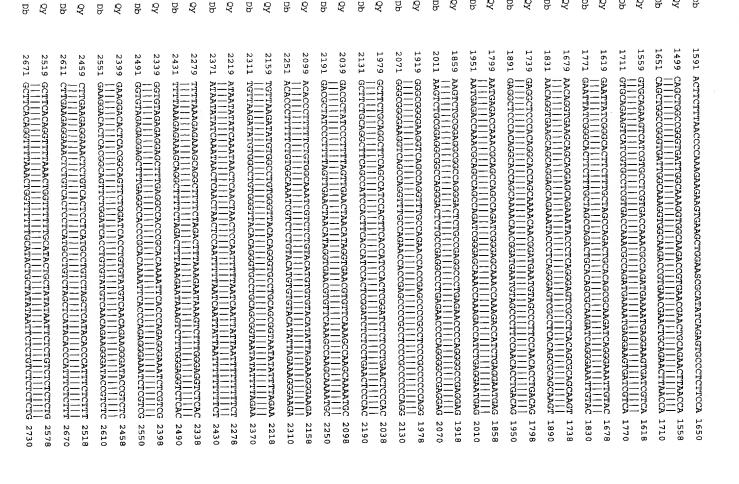
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AAS26153 standard; CDNA; 2290 ВР

AAS26153

07-NOV-2001 (first entry)

CDNA encoding a novel secreted protein, Seq ID 332

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives.
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                    AGCGCAGCAAGTGAGGCTCCCACAGGCACCAGCAAAACAACGGATGAATGTAGCCCTTCC
                                                                                                GGGAAATTGTACAACAGGTGAAGCAGCAGCAGCAGAAATACCCTCAGGGAGTCGCCTCAC
                                                                                                                                                                AAGTGATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCA
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                                                                     GGGAAATTGTACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCAC
                                                                                                                                             AAGTGATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCA
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New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or renal disorders. S,

English.

The invention relates to human novel polypeptides and their associated CC polynucleotides. The polypeptides and polynucleotides are useful in gene CC therapy for treating, inhibiting or preventing neural disorders, immune CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g. cand multiple sclerosis), muscular disorders, respiratory diseases (e.g. cand multiple sclerosis), muscular disorders, respiratory diseases (e.g. cand multiple sclerosis), muscular disorders, respiratory diseases (e.g. congenital disorders, pulmonary disorders, cardiovascular disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage crenal disease), hyperproliferative disorders (e.g. Hodykin's disease and cleukaemia), inflammatory diseases (e.g. septic shock, bursitis and capendicitis), allergic reactions and conditions (e.g. asthma), blood crelated disorders (e.g. thrombosis, atherosclerosis and myocardial cc infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent creations conditions cand condition conditions and conditions con

Sequence 2290 B₽; 707 A; 561 c; 491 G 531 Τ; 0 ₽, 0 Other;

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Best Local Simi
Matches 2028;
1247 CCCAGGCTGTGGGCGCATCATCGGGAAGAAGGGGGGCACACATCAAACAGCTGGCGAGAT
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                                     60.6%;
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Pred. No. 0;
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	327 GGGAGGTCTCACGGTGTAGAGAGGAGCTTTGAGGC
	2267 ATTITITITCTTTTAAAGAGAAAGCAGGCTTTTCTAGACTTTAAAGAATAAAGTCTTT 2326
	2207 TATATTTTAGAAATAATATKAACAAATAACTCAACTAACTCCAATTTTAATCAATTATTA
	2147 AGAAAGGGAAGATGTTAAGATATGTGGCCTGTGGGTTACACAGGGTGCCTGCAGCGGTAA 2206
	2087 CAAGCAAAATGCACACCCTTTTTCTGTGGCAAATCGTCTCTGTACATGTGTGTACATATT 2146
	2027 CTGAACTCCCACGACGCTATCCCTTTTAGTTGAACTAACATAGGTGAACGTGTTCAAAGC 2086
	1967 CCGCCCCCAGGGCTTCTGCAGGCTTCAGCCATCCACTCCACTCGACTCGGATCTCTC 2026
,	1907 GGGGCCGAGGAGGGGGGGAAGGTCAGCCAGGTTTGCCAGAACCACCGAGCCCCGCCTC 1966
	1847 CTGAGGAATGAGAAGTCTGCGGAGGCGAGGGCCAGGGACTCTGCCGAGGCCCTGAGAACCCCA 1906
	1787 AACACCTGACAGAATGAGACCAAAACGCAGCCAGATCGGGAGCAAACCAAAGACCAT 1846
	1727 AGCGCAGCAAGTGAGGCTCCCACAGGCACCAGCAAAACAACGGATGAATGTAGCCCTTCC 1786
	1667 GGGAAATTGTACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGGTCGCCTCAC 1726
	1607 AAGTGATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCA 1666
	1547 AGAACTTAACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGG 1606
	1487 TGCCCTCTTCCACAGCTGGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGAAC
	1427 TGAAAGAGGAAAAACTTCTTTAACCCCAAAGAAGAAGTGAAGCTGAAGCGCATATCAGAG 1486
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	1307 TCGCCGGAGCCTCTATCAAGATTGCCCCTGCGGAAGGCCCCAGACGTCAGCGAAAGGATGG 1366
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RESULT 9
AAS70981
ID AAS7
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AC AAS7
XX
DT 13-F
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DE DNA
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DE Huma

AAS70981 standard; cDNA; 2010 BP

13-FEB-2002 (first entry)

DNA encoding novel human diagnostic protein #6785

Human; chromosome mapping; gene mapping; gene therapy; forensic;

food

supplement;

88

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CC genes. (1) is useful in gene therapy techniques to restore normal CC activity of (II) or to treat disease states involving (II). (II) is CC useful for generating antibodies against it, detecting or quantitating a CC useful for generating and its against it, detecting or quantitating a CC polypeptide in tissue, as molecular weight markers and as a food CC supplement. (II) and its binding partners are useful in medical imaging CC stype the styressing (II). (I) and (II) are useful for treating disorders involving abservant protein expression or biological activity. The CC polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC coding sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this constant did not appear in the printed specification, but was obtained in CC ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 1858; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also use in diagnostics as expressed sequence tags for identifying expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutatio diagnosible for genetic disorders or other traits and to assess
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                                                          ACTGGGCCATCGGCGCCATCGAGACCCTCTCGGGTAAAGTGGAATTGCATGGGAAAATCA
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24-OCT-2001; 2001US-0343629P.
29-OCT-2001; 2001US-0349575P.
01-WOV-2001; 2001US-0346557P.
25-JUN-2002; 2002US-03931342P.
01-OCT-2002; 2002US-00262445.
                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes an isolated polypeptide comprising any of 33 90 1273 amino acid sequences (I) given in the specification or its mature form, a sequence that is at least 95 % identical to (I), or a sequence comprising one or more conservative substitutions in the amino acid sequence of (I). The polypeptide is useful for preparing a composition for treating or preventing e.g. cancer. This sequence encodes a novel
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Gerlach VL, Gir
Tet I, Ooi CF
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Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostaticardiant; vasotropic; cerebroprotective; noctropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food addit preservative; antiproliferative.
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2000US-0231413P.
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2000US-0232080P.
2000US-0232081P.

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C(ELISA). Disorders which are diagnosed or treated include autoimmune (CELISA). Disorders which are diagnosed or treated include autoimmune (CELISA). Disorders e.g. rheumatoid arthritis, hyperproliferative disorders e.g. caroplasms of the breast or liver, cardiovascular disorders e.g. cardiac (CELISA) cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, CELISA, viruses and fungi and ocular disorders e.g. corneal infection, CELISA, viruses and fungi and ocular disorders e.g. corneal infection, CELISA, viruses and fungi and ocular disorders e.g. corneal infection, CELISA, viruses and fungi and cellar prolification. The polypeptides (CELISA) can also be used to aid wound healing and epithelial cell proliferation, CELISA, can also be used to aid wound healing and epithelial cell proliferation, CELISA, can also be used to aid wound healing and epithelial cell proliferation, CELISA, can also be used (CELISA) contents, for supporting cell culture of primary tissues, to CELISA, can also be used (CELISA) content, lipid, protein, carabohydrate, vitamins, capabilities, fat content, lipid, protein, carabohydrate, vitamins, capabilities, fat content, lipid, protein, carabohydrate, vitamins, capabilities, can also be used (CELISA) contents. The present (CELISA) contents and other mutritional components. The present (CELISA) contents and content did not form part of the printed (CELISA) contents and content did not form part of the printed (CELISA).
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17-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosophanit assays pricated in the condition of the protein can be used in the condition of the protein and the protein can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosophanit assays importance which was a diagnostic pricated in the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the prot
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                                           CCCAGGCTGTGGGGCCATCATCGGGAAGAAGGGGGGCACACATCAAACAGCTGGCGAGAT 1306
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eural disorder; immune system disorder; renal disorder; respiratory disease; reproductive disorder; isorder; pulmonary disorder; cardiovascular disorder; disorder; inflammatory disease; allergic reaction; rder; cancer; immunosuppressive; antiinflammatory; phrotropic; cytostatic; antiallergic; thrombolytic; rteriosclerotic.

S-0179055P S-0118086P S-0214808P S-0216647P S-0217487P S-0217487P S-0221964P S-0224519P S-0225276P S-0225276P S-0225276P S-02257575P S-0225758P S-0225758P S-0225758P S-0225758P S-0225758P S-0225759P S-0225758P S-0225759P S-0236379P S-0236379P S-0236379P S-02363703PP S-0237038P S-0237039P S-0237039P S-0237039P S-0237039P S-0237039P S-0237039P S-0237039P -00764864

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                 AAGTGATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCA
                                                                                         AGAACTTAACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGG
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 AAGTGATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCA
                                                             AGAACTTAACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGG
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                                                                          TTGGGAGGTCTCACCGTGTAGAGAGGAGCTTTGAGGCCACCCGCACAAAATTCACCCAGA
                                                                                                            TAATTTTTTTTTTTTAAAGAGRAAGCMGGCTTTTCTAGACTTTAAAGAATAAAGTCT
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RESULT 13
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XX 21-FE
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XX Lung
KW Vacci
XX Vacci
XX U0200
XX U0200
XX Homo
PN W0200
XX Y0200
AAC66035 standard; cDNA; 1740

21-FEB-2001

(first

entry)

Human lung cancer-associated cDNA antigen L523S

Lung cancer; therapy; vaccine; detection; ss treatment; human; tumor; immunogenic; cytostatic;

Homo sapiens

WO200061612-A2

03-APR-2000;

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Matches 1116;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit development of cancer
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17-DEC-1999;
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02-AUG-2000;
21-AUG-2000;
15-SEP-2000;
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                                                                                                                                                                                                                                                                                The present invention describes human lung tumour proteins. Human lung tumour proteins and polynuclectides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynuclectides, antibodies, fusion proteins, Teell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABI48959 to ABI49300 and ABB74946 to ABB75770 represent sequences used in the exemplification of the present
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be Y, Peckham DW, Cai F,
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Novel lung carcinoma polynucleotide sequences and polypeptides encoded the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer. γď

Claim 1; Page 337; 381pp; English.

comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the oligonucleotide to a predetermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABQ92145 to ABB92486 and ABP61866 to ABP61992 represent sequences used in the exemplification of the present invention. The present invention describes isolated human lung carcinoma polypucleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions

Sequence 1740 B₽; 526 A; 406 C; 417 G; 391 T; 0 ₫, 0 Other;

Query Match Best Local S Matches 1116

Similarity

21.2%;

Score 697.2; DB 6; Pred. No. 2.1e-174; Mismatches

DB 6; 538;

1740; 66;

1116;

Conservative

0;

Indels Length

Gaps

멍 Ş 뭐 8 g Ş 밁 Ś 문 Š 밁 8 밁 Ş 밁 8 601 421 361 301 373 241 181 313 121 193 133 61 73 Н CTGGTTCCCACCCAATTTGTTGGAGCCATCATAGGAAAAGAAGGTGCCACCATTCGGAAC CTGGTCCCCACCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGAAC GTTGTCAACGTCACATATGCAACAAGAAGAAGAAGCAAAAATAGCCATGGAGAAGCTAAGC CTAGTCCAGTATGGAGTGGTGGAGAGCTGTGAGCAAGTGAACACTGACTCGGAAACTGCA AGGCAGGGGTCTCCAGGATCCGTATCCAAGCAGAAACCATGTGATTTGCCTCTGCGCCTG -----CACGCCCTGGGGGCACTTCTCAGGCCAGACAGATTGATTTCCCGCTGCGGATC CAGCAAAACCCCTTGCAGCAGCCCCGAGGTCGCCGGGGGCTTGGGCAGAGGGGCTCCTCA TCCCCTTCGCCCCTCAGCGAGCCCAGCGTGGGGACCACTCTTCCCGGGAGCAAGGC---GGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGATGAAGAGGTGAGC CGGAAACTTCAGATACGAAATATCCCCGCCTCATTTACAGTGGGAGGTGCTGGATAGTTTA ATAGAACTGCACGGGAAACCCATAGAAGTTGAGCACTCGGTCCCAAAAAGGCAAAGGATT GTGGAATTGCATGGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAAGCTAAGGAGC ATCTTCAAGGACGCCAAGATCCCGGGTGTCGGGACCCTTCCTGGTGAAGACTGGCTACGCG CTCTTTGGGGACAGGAAGCTGCCCCTGGCGGGACAGGTCCTGCAAGTCCCGGCTACGCC GGATTTCAGTTAGAGAATTTCACCTTGAAAGTAGCCTATATCCCTGATGAAAACGGCCGCC GTTGTAAATGTAACCTATTCCAGTAAGGACCAAGCTAGACAAGCACTAGACAAACTGAAT ттостедастассссанссадаастедессатссвеессатсвавассстстсвеетала ATGAACAAGCTTTACATCGGGAACCTGAGCCCCGCCGTCACCGCCGACGACCTCCGGCAG TTCGTGGACTGCCCGGACGAGAGCTGGGCCCTCAAGGCCATCGAGGCGCTTTCAGGTAAA 999 723 360 372 600 663 540 480 420 492 120 192 609 300 240 312 180 252 60 132

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7 AAGCAGCAGGAGCAGAATACCCTCAGGGAGTCGCCTCAC 1726 	1687 AA 1681 AA
7 GGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCAGGGAAATTGTACAACAGGTG 1686 	1627 GG 1621 GG
7 GTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTCAGAATTAIC 1626	1567 GT 1561 GT
	1507 CG 1501 AG
7 AACCCCAAAGAAGAAGTGAAGCTGGAAGGGCATATCAGAGTGCCCTCTTCCACAGCTGGC 1506 	1447 AA 1441 AG
7 GAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAAGAGGAAAACTTCTTT 1446 	1387 GA 1381 GA
7 ATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCACCAGCGGCCCACCG 1386	1327 AT 1321 AT
ATCGGGAAGAAGGGGGCACACATCAAACAGCTGGCGAGATTCGCCGGAGCCTCTATCAAG 1326	267 261
TTATCCAGAGCAGGAGATTGTGAATCTCTTCATCCCAACCCAGGCTGTGG	1209'
GCCTGTACCCCCATCACCAGTTTGGCCCGTTCCCGCATCATCACTC	1163 GC 1141 GG
ACTTCT 	1144 CAO 1081 CAO
GCTGCGTGAGGCCTTTGAAAATGATATGCTGGC 	1084 ATA 1021 GA
TACAACCCGGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCTGAG 1083	1024 TAC
AAAATTGAACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATA 1023	964 AAJ 901 AAJ
ATCTTGGCACACAATGGCTTGGTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTGAAG 963 	904 ATO 841 ATT
CTTGAAATCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAAA 903 	844 CTT
GAGAAGCCTGTCACCATGCCATGCCACAGAGGGGACTTCTGAAGCATGCCGCATGATT 843	784 GAG 721 GAG
ATCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAAACTCTGGAGCTGCA 783	724 ATC 661 ATC

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Search completed: July 24, 2004, 07:28:53 Job time : 1231.37 secs

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Copyright (c) 1993 - 2004 Compugen
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APPLICANT: Gure, Ali
APPLICANT: Gure, Ali
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Jager, Elke
APPLICANT: Hauth, Alexander
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Isolated Nucleic Acid Mol
TITLE OF INVENTION: Antigen, The Antigens Per
FILE REFERENCE: LUD 5538
CUGRENT APPLICATION NUMBER: US/09/061,709B
CUGRENT FILING DATE: 1998-04-17
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Best Local Similarity
Matches 3283; Conserv
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LENGTH: 3283
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ORGANISM: Homo
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RESULT 2
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(Sequence 8, Application US/09899651
Patent No. 6576756

(GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng
APPLICANT: Gure, Ali
APPLICANT: Stockert, Elisabeth
APPLICANT: Jager, Elke
APPLICANT: Jager, Elke
APPLICANT: Holyd J.

(TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cance of Invention Associated
TITLE OF INVENTION: Associated
CURRENT APPLICATION UNMBER: US/09/899,651
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US/09/861,709
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1731 1860	572 ATTGTACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGGGC 	
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; Sequence 6, Application US/09899651

; Patent No. 6576756

; GENERAL INFORMATION:

APPLICANT: Chen, Yao-Tseng

; APPLICANT: Tsang, Solam

APPLICANT: Stockert, Elisabeth

; APPLICANT: Jager, Elke

; APPLICANT: Old, Lloyd J.

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer

TITLE OF INVENTION: Associated

; TITLE OF INVENTION: Annigen, The Antigens Per Se, And Uses Thereof

; TITLE REFERENCE: LUD 5538

; CURRENT APPLICATION NUMBER: US/09/899,651

; CURRENT FILING DATE: 2001-07-06

; PRIOR APPLICATION NUMBER: US/09/061,709

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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 347
LENGTH: 1740
TYPE: DNA
ORGANISM: Homo sapiens
US-09-643-597-347
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US-09-643-597-347
; Sequence 347, Application
; Patent No. 6426072
; GENERAL INFORMATION:
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Best Local Similarity 64.9%;
Matches 1116; Conservative
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Pred. No. 4.8e-185;
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; TYPE: DNA
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US-09-542-615A-347
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APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: FADGER, GATY R.
APPLICANT: Hosken, Nancy A.
APPLICANT: COMPOUNDS AND METHODS FO TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Wang, To
APPLICANT: Fan, Liq
APPLICANT: Kalos, M:
APPLICANT: Bangur,
APPLICANT: Bangur,
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Best Local Similarity 64.9%;
Matches 1116; Conservative
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Fan, Liqun
Kalos, Michael D.
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                                                           ATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCATCACGGGCCACCG
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APPLICANT: KAIOS, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
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COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT APPLICATION NUMBER: US/09/606,421B
NUMBER OF SEQ ID NOS: 358
NUMBER OF SEQ ID NOS: 358
SOFTMARE: FASTSEE FOR Windows Version 3.0
SEQ ID NO 347
LENGTH: 1740
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                                                                                                                                                                                                                                                                                                      Query Match 21.2%; Score 697.2; DB 4; Best Local Similarity 64.9%; Pred. No. 4.8e-185; Matches 1116; Conservative 0; Mismatches 538;
                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
-09-606-421B-347
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                    TTCGTGGACTACCCCGAGACCAGAACTGGGCCATCCGCGCCATCGAGACCCTCTCGGGTAAA
ATAGAACTGCACGGGAAACCCATAGAAGTTGAGCACTCGGTCCCAAAAAGGCAAAGGATT 240
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APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
APPLICANT: Gure, Ali
APPLICANT: Tsang, Solam
APPLICANT: Stockert, Elisabeth
APPLICANT: Jager, Elke
APPLICANT: Jager, Elke
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
FILE REFERENCE: LUD 5538
CURRENT APPLICATION NUMBER: US/09/061,709B
CURRENT FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
TYPE: DNA
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Matches 1115; Conservative
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ATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCACCGGGGCCACCG 1386
                                     ATCGGCAAGCAGGCCAGCACATCAAGCAGCTTTCTCGCTTTGCTGGAGCTTCAATTAAG
                                                                           ATCGGGAAGAAGGGGGCACACATCAAACAGCTGGCGAGATTCGCCGGAGCCTCTATCAAG
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APPLICANT: Tsang, Solam
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APPLICANT: Stockert, Elisabeth
APPLICANT: Mager, Elke
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Alexander
APPLICATION: Associated
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
FILE REFERENCE: LUD 5538
CURRENT APPLICATION NUMBER: US/09/899,651
CURRENT TILING DATE: 2001-07-06
PRIOR APPLICATION UNMBER: US/09/061,709
PRIOR FILING DATE: 1998-04-17
DRIOR FILING DATE: 1998-04-17
DRIOR FILING DATE: 1998-04-17
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Best Local Sim
Matches 1115;
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Patent No. 6576756
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LENGTH: 4159
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APPLICANT: Gure, Ali
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                                                                                                              ATCTTCAAGGACGCCAAGATCCCGGTGTCGGGACCCTTCCTGGTGAAGACTGGCTACGCG 370
                                                                                                                                                                                       ATGAACAAACTGTATATCGGAAACCTCAGCGAGAACGCCGCCCCCTCGGACCTAGAAAGT 310
 GTGGAATTGCATGGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAAGCTAAGGAGC
                                                             TTCGTGGACTACCCCGACAAACTGGGCCATCCGCGCCATCGAGACCCTCTCGGGTAAA
                                                                                                                                               CTCTTTGGGGACAGGAAGCTGCCCTGGCGGGACAGGTCCTGCTGAAGTCCGGCTACGCC 192
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                                      TTCGTGGACTGCCCGGACGAGAGCTGGGCCCTCAAGGCCATCGAGGCGCTTTCAGGTAAA
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ATCGGGAAGAAGGGGGCACACCAACCAAGCTGGCGAGATTCGCCGGAGCCTCTATCAAG
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GENERAL INFORMATION:

APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Anichael D.

APPLICANT: Walos, Michael D.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Hosken, Nancy

APPLICANT: Hanger, Gary R.

APPLICANT: Wang, Anjun

APPLICANT: Wang, Anjun

APPLICANT: Menetson, Robert A.

APPLICANT: Menetson, Robert A.

APPLICANT: MCNeill, Patricia D.

TITLE OF INVENTION: COMPOSITIONS AND METHOD

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG COMPOSITION AND PRICE US/09/643,597

CURRENT APPLICATION NUMBER: US/09/643,597

CURRENT FILING DATE: 2000-08-21
                                                                                                                                                                                                                    LENGTH: 4181
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FATURE:
NAME/KEY: unsure
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NAME/KEY: unsure
LOCATION: (3502)
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LOCATION: (3506)
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OTHER INFORMATION: 1
NAME/KEY: unsure
LOCATION: (3520)
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NAME/KEY: unsure
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APPLICANT: Wang, Tongtong
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
ITITLE OF INVENTION: COMPOUNDS AND METHODS FOR ITITLE OF INVENTION: AND DIAGNOSIS OF LUNG CRETENT APPLICATION NUMBER: US/09/480,884A
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
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LENGTH: 4181
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LOCATION: (3502,
OTHER INFORMATION: 7
NAME/KEY: unsure
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(3506)
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TITLE OF INVENTION: AND DIAGNOSIS
TITLE OF INVENTION: AND DIAGNOSIS
TITLE OF EMPERENCE: 210121.455C8
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LOCATION: (3646)
OTHER INFORMATION: I
NAME/KEY: unsure
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OTHER INFORMATION: 1
NAME/KEY: unsure
LOCATION: (3974)
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OTHER INFORMATION:
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Kalos, Michael D.
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LOCATION: (4080)
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                         CTGGAGATTATGCATAAGGAAGCTCAAGATATAAAATTCACAGAAGAGATCCCCTTGAAG 1090
                                                      СТТGАААТСАТGСАGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAAA 903
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Sequence 175, Application US/09606421B
Patent No. 6531315
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Hosken, Nancy
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Fanger, Gary R.
Li, Samuel X.
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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION UNMERR: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 175
                                                                                                                                                                                         FEATURE:

NAME/KEY: unsure

(4036)
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NAME/KEY: unsure
LOCATION: (3968)
OTHER INFORMATION: 1
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NAME/KEY: unsure
LOCATION: (3940)
OTHER INFORMATION: 1
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NAME/KEY: unsure
NAME/KEY: (3520)
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(3502)
          NAME/KEY: unsure LOCATION: (4088)
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NAME/KEY: unsure
LOCATION: (3347)
OTHER INFORMATION: 1
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: (3538)
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LOCATION: (3506)
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TYPE: DNA
ORGANISM: Homo sapiens
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; FEATURE:
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                     AAAATTGAACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATA
                                                  ATCTTGGCACACAATGGCTTGGTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTGAAG
                                                                                                      CTGGAGATTATGCATAAGGAAGCTCAAGATATAAAATTCACAGAAGAGATCCCCTTGAAG
                                                                                                                      CTTGAAATCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCCTCTGAAA
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 <u>AAAATTGAGCAAGACACAGACACTAAAATCACGATATCTCCATTGCAGGAATTGACGCTG</u>
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Pred. No. 2.6e-184;
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Sequence 1, Application US/09261855A
Patent No. 6255055
GENERAL INFORMATION:
APPLICANT: ROSE, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION I
TITLE OF INVENTION: (CKD-BP) AND ITS NUCLEIC
FILE REFERENCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2224
TYPE: DNA
ORGANISM: Mus musculus
US-09-261-855-1
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REGION DETERMINANT-BINDING NUCLEIC ACID SEQUENCE

PROTEIN

RESULT 14 US-09-261-855-1

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Query Match
Best Local Similarity
Matches 1117; Conser
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Pred. No. 1.5e-181;
0; Mismatches 560;
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                                                                APPLICANT: Chen, Yao-Tseng
APPLICANT: Gure, Ali
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Muth, Alexander
APPLICANT: Muth, Alexander
APPLICANT: Muth, Alexander
APPLICANT: Lold, Lloyd J.
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer As
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
FILE REFERENCE: LUD 5538
CURRENT APPLICATION NUMBER: US/09/061,709B
CURRENT FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
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GENERAL INFORMATION:
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----CTTATCCAGAGCAGGAGATTGTGAATCTCTTCATCCCAACCCAGGCTGTGGGCGC 1262
                                                                                                              CCCCATCACCAGTTTGGCCCGTTCCCGCATCATCACT---
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p	1064	TATGCAGGCTCCCGAGCAGGAGATGGTGCAGGTGTTTATCCCCGCCCAGGCAGTGGGCGC 1123
γQ	1263	CATCATCGGGAAGAAGGGGCCACACATCAAACAGCTGGCGAGATTCGGCGGAGCCTCTAT 1322
Db	1124	CATCATCGGCAAGAAGGGGCAGACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCAT 1183
Qy Qy	1323	CAAGATTGCCCCTGCGGAAGGCCCCAGACGTCAGCGAAAGGATGGTCATCACCGGGCC 1382
Дb	1184	CANGATTGCACCACCCGAAACACCTGACTCCAAAGTTCGTATGGTTATCACTGGACC 1243
VΩ	1383	ACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAAGAGGAAAACTT 1442
Вb	1244	GCCAGAGGCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTT 1303
Ϋ́	1443	CTTTAACCCCAAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACAGC 1502
Db	1304	CTTTGGTCCCAAGGAAGTGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGC 1363
Qγ	1503	TGGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGAAC
Db	1364	TGGCCGGGTCATTGGCAAAAGGTGGAAAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGC 1423
ΥQ	1563	AGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTCAGAAT 1622
Db	1424	TGAGGTGGTAGTACCAAGAGACCAGACCCCTGATGAGAACGACCAGGTCATCGTGAAAAT 1483
Qy	1623	TATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCAGGGAAATTGTACAACA 1682
Db	1484	CATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGAAGATCCGAGACATCCTGGCCCA 1543
Qy	1683	GGTGAAGCAGCAGGAGCAGAAATACCCCTCAGGGAGTCGCCTCACAGGGGAAGCAAGTGAGG 1742
Db	1544	GGTTAAGCAGCAGCATCAGAAGGGACAGAGTAACCAGGCCCAGGCACGGAGGAAGTGACC 1603
Ş	1743	CTCCC 1747

Search completed: July 24, 2004, 16:48:44 Job time : 248.862 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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sequence 347, App	ddw '/ FC acrember	1.				Sequence 749, App			Sequence 329, App	Sequence 6, Appli	Sequence 48, Appl	Sequence 146, App	Sequence 20241, A	Sequence 8, Appli	Description	

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09899651
Patent No. US20020111470A1
                                                                                                                   Matches 3283;
                                                                                                                                     Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Stockert, Elisabeth
APPLICANT: Jager, Elke
APPLICANT: Jager, Elke
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
FILE REFERENCE: LUD 5538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/899,651
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US/09/061,709
PRIOR FILING DATE: 1998-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chen, Yao-Tseng
                                                                                                                                                                                                                           LENGTH: 3283
TYPE: DNA
ORGANISM: Homo sapiens
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61 AAGAGACGGATGATGAACAAGCTTTACATCGGGAACCTGAGCCCCGCCGTCACCGCCGAC
                                                         1 GGCAGCGGAGGAGCGCGAGGAGCCCCGGGTACCGGGGCCGGGGGAGCCGGGGGTCTCCGGGG
                                                                                                           h 100.0%; Score 3282; Similarity 100.0%; Pred. No. 0; 83; Conservative 0; Mismatches
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121 GACCITCOGGCACCCTTTTTGGGGACACGACCACACACGACCCCCCCC
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Sequence 20241, Application

US/09814353

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APPLICANT: Lee, John
APPLICANT: Lee, John
APPLICANT: Lee, John
APPLICANT: Lillie, James
ITITE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
ITITE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
ITITE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
ITITE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/291,031
PRIOR FILING DATE: 2000-03-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR APPLICATION NUMBER: US 60/257,672
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; LOCATION: 1, 3897, 3898, 3899, 3900, 3901, 3902, 3903, 3904, 3905
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-20241
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Best Local
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                          AGAAACCGCCGTTGTCAACGTCACATATGCAACAAGAGAAGAAGAAGCAAAAATAGCCATGGA
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Pred. No. 0;
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APPLICANT: Xunei ZHAO

APPLICANT: Karen GLATT

IIILE OF INVENTION: Nucleic Acid Molecules and Proteins For The TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ova: CURRENT APPLICATION NUMBER: US/10/097,340

CURRENT FILING DATE: 2002-03-14

PRIOR APPLICATION NUMBER: 60/276,025

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/325,149

PRIOR APPLICATION NUMBER: 60/276,026

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US-10-097-340-146
; Sequence 146, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
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APPLICANT: Manjula GANNA
APPLICANT: Sebastian HOEI
APPLICANT: Shubhangi KAM
APPLICANT: Steve G. KOVA:
APPLICANT: Rachel E. MEYN
APPLICANT: Michael MORRIS
APPLICANT: Michael MORRIS
APPLICANT: Michael MORRIS
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Peter VEIBY
APPLICANT: Robert C. BAST
                                                                                                                                                                                                                                APPLICANT:
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Peter VEIBY
Gordon B. MILLS
Robert C. BAST, Jr.
Karen LU
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Rachel E. MEYERS
Michael MORRISEY
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Shubhangi KAMATKAR
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PRIOR FILING DATE: 2001/09/26
PRIOR FILING DATE: 2001-08-10
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PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
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Similarity 99.8%;
 AGAGAAGCCTGTCACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATGAT
                                                  CATCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCTGGAGCTGC
                                                                                                  CCTGGTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGAA
                                                                                                                     CCTGGTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGAA
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QY 303 GCTAAGGAGCAGGAAAATTCAGAATTCGAAACATCCCTCCTCACCTGCAGTGGGAGGTGTT 362	Qy 243 CTCGGGTAAAGTGGAATTGCATGGGAAAATCATGGAAGTTGATTACTCAGTCTGTAAAAA 302	Qy 183 CGCCTACGCCTTCGTGGACTACCCCGACCAGAACTGGGCCATCCGCGCCATCGAGACCCT 242	Oy 123 CCTCCGGCAGCTCTTTGGGGACAGGAAGCTGCCCCTGGCGGGACAGGTCCTGCTGAAGTC 182	OY 63 GAGACGGATGAACAAGCTTTACATCGGGAACCTGAGCCCCGTCACCGCCGACGA 122	CGGGGAAGCCGCGGGCTCTCGGGGAA 62	Query Match 99.1%; Score 3253.8; DB 17; Length 3667; Best Local Similarity 99.8%; Pred. No. 0; Matches 3277; Conservative 0; Mismatches 3; Indels 2; Gaps 2;		NUMBER OF SEQ ID NOS: 557 SOFTWARE: Patentin version 3.2 SEQ ID NO 48		; APPLICANY: BIISTOL-Myers Squibb Company ; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT ; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR ; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS	O m to i	RESULT 4		CCAAGAAC	Db 3488 TTTTTATTTATTAAAAATGAAGTTGGAAAAAAAATAAGATATCAACTGCCAGCCTGG 3181	3428 CTCAGCACCTTGATCTTTTTTTTTTTTTTTTTTTTTTTT	30	TGTTTTTAC
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2223 TATATCANATAACTCAACTACTCCAATTTTTAATCAATTATTATTTTTT	1503 TESCCOGGETCALIGNAGAGAGACCEGAAGCGCATATCAGAGTGCCCCCTCTCCCAGC 1868 1503 TESCCOGGETCALTGGCAAAGGTGGCAAACCGCAACTGCAGACTTAACCAGTGC 1562 11869 TESCCOGGETCALTTGGCAAAGGTGGCAAACCGCAACTGCAACTGCAGACTTAACCAGTGC 1528 1563 AGAAGTCATCGTGCCTCCTTGCCAACCGCAAACCGCAAATGAGAAATGAGGAAATTGTAACCAGTGC 1528 1563 TATCGGGCATTCTTTGCCAAACCGCAGATGAAAATGAGGAAATTGATCAGAAT 1622 11919 AGAAGTCATCGTGCCTTGCTTAGCCAGACTGCACAGCGCCAAATGAGGAAATTGATCAACAT 1588 1623 TATCGGGCACTTCTTTGCTAACCAAACCCCAGATGAAAATGAGGAAAATTGATCAACAT 1588 1623 TATCGGGCACTTCTTTGCTAGCCAAACCCCAGATGAAAATGAGGAAAATTGATCAACAT 1588 1624 TATCGGGCACTTCTTTGCTAGCCAAAACCCCTCAGGGAAAATGAGGAAAATTGATCAACA 2048 1683 GGTGAAGCAGAGAAAAAACACCACAAACCCTCAAGAGTCAACCCTGACAAACTTGACAACAT 2048 1683 GGTGAAAGCAGGAAAAAAAACACACGAAATGAGCCAAACACCTGACAAACTTGACAAACTTGACAAACTTGACAAACTTGACAAACTTGACAAACTTGACAAACTTGACAAACTTGACAAACTTGACAAACTTGACAAACTTGACAAACTTGACAAACTTGACAAAACTTGACAAACTTGACAAACTTGACAAAACTTGACAAAACTTGACAAAACTTGACAAAACTTGACAAAACTTACAAACTTACAAAACTTACAAAACCAAACCAAAACCAAAACCAAAACCAAAACCAAAA
RESULT 5 US-09-659-651-6 US-09-659-651-6 ; Sequence 6, Application US/09899651 ; Patent No. US20020111470A1 ; Patent No. Isolated No. Isolated No. Isolated No. Isolated No. Isolated No. Isolated TITLE OF INVENTION: Associated TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof FILE REFERENCE: LUD 5538 ; CURRENT FILING DATE: 2001-07-06 ; PRIOR APPLICATION NUMBER: US/09/899,651 ; CURRENT FILING DATE: 2001-07-06 ; PRIOR FILING DATE: 1998-04-17 ; NUMBER OF SEQ ID NOS: 8 ; SEQ ID NO 6 ; LENGTH: 3412	Oy 2583 TCTCTCCCCTCCCCTCCCCTTCCTCTCTCCATTCTTTTTGAATTTCCTCATCC 2642 2643 CTCCATCTCAATCCCCTACCCTTCCTCTCTCCATTCTTTTTGAATTTCCTCATCC 2642 2643 CTCCATCTCAATCCCCTACCCTCCCCTCCCCCCCCCCC

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Qy 1852 GAATGAGAAGTCTGCGGAGGCCCAGGGACTCTGCCGAGGCCCTGAGAACCCCAGGGGC 1911	Qy 1792 CTGACAGAATGAGACCAAACGCAGCCAGACCAGATCGGGAGCAAAGCCAAAGACCATCTGAG 1851	1 2	1672 1801	1612 1741	Qy 1552 TTAACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTG 1611	Qy 1492 TCTTCCACAGCTGGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGAAC	Qy 1432 GAGGAAAACTTCTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCC 1491	1372 1501	1312 1441	Qy 1252 GCTGTGGGGGCCATCATCGGGAAGAAGGGGGCACACATCAAACAGCTGGCGAGATTCGCC 1311	1192 1321	11 41 1261	1141 1201 CTGTCCGTG	11	10	1021 1021	Oy 961 AAGAAAATTGAACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGC 1020

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GENERAL INFORMATION:
APPLICANT: Rosen et al.
FILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 329
LENGTH: 3694
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity 96.0
Matches 3214; Conservative
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Query Match 60.6%; Score 1989.8; DB 9; Length 2290; Best Local Similarity 99.4%; Pred. No. 0; Matches 2028; Conservative 0; Mismatches 8; Indels 4; Gaps 3; Matches 2028; Conservative 0; Mismatches 8; Indels 4; Gaps 3; Qy 1247 CCCAGGCTGTGGGGCCATCATCATCGGGAAGAAGGGGGGCACACCATCAACAGCTGGCGAGAT 1306 Qy 1247 CCCAGGCTGTGGGCCCATCATCATCAGCGGGAAGACACCATCAACAGCTGGCGAGAT 1306	; Prior application data removed - consult Falm of the widge; ; NUMBER OF SEQ ID NOS: 1792 ; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 332 ; LENGTH: 2290 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-764-864-332	ids, Proteins, and Antib	RESULT 7 US-09-764-864-332 ; Sequence 332, Application US/09764864 ; Patent No. US20020132753A1	Qy 3236 AAGAACCNATATGGCCTTCTTTTGGACAAACCTTGAAAATGTTTATTT 3283 	QY 3176 GCCTGGAGAAGGTGACAGTCCAAGTGTGCAACAGCTGTTCTGAATTGTCTTCCGCTAGCC 3235	3116	ATAGTTGG			Db 2971 AACAGGAACCAACCAAACCAAACAAAGAAAAAAATTCAACAAAGAAGAAGAAAAAATTCACACAATGAAAGA 3030 Qy 2877 ATGTTTTTTTTTTGCATTTTTGGTATAAAGCCATCAATATTCAGCAAAATGATTCC 2936	Db 2911 ACTTGGTTACTCAAAAGAACAAGAGTCAATGGTACTTGTCCTAGCGTTTTGGAAGAGAA 2970 Qy 2817 AACAGGAACCACCAAACCAACCAACCAAACAAAAAAATTCCACAATGAAAGA Qy 2817 AACAGGAACCAACCAACCAACCAACCAAACAAAAAATTCCACAATGAAAGA	2851 2757	N N I	Db 2731 TITATCTCTCCCCTCCCCTCCCCTTCTTCTCCATCTCCATCTTTTGAATTTCCTC 2790 00 2639 ATCCCTCCGTTCAATCCCCTATCTACGCACCCCCCCCCC
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TYPE: DNA
CORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (5)..(1669)
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PRIOR APPLICATION NUMBER: 60/341,058
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/343,629
PRIOR FILING DATE: 2001-10-24
PRIOR PPLICATION NUMBER: 60/349,575
PRIOR FILING DATE: 2001-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/327, 454
PRIOR PILLING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/327, 917
PRIOR APPLICATION NUMBER: 60/328, 029
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328, 056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328, 849
PRIOR APPLICATION NUMBER: 60/328, 849
PRIOR APPLICATION NUMBER: 60/329, 414
PRIOR APPLICATION NUMBER: 60/329, 414
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NUMBER OF SEQ ID NOS: 133
SOFTWARE: CuraSeqList version
SEQ ID NO 39
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Best Local Similarity
Matches 1624; Conserv
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CURRENT APPLICATION NUMBER: US/10/262,
CURRENT FILING DATE: 2002-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS TITLE OF INVENTION: THE SAME
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FILING DATE: 2001-10-09
APPLICATION NUMBER: 60/328,849
FILING DATE: 2001-10-12
APPLICATION NUMBER: 60/329,414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2001-10-15
APPLICATION NUMBER: 60/330,142
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                                                                                     GGGTAAAGTGGAATTGCATGGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAAGCT
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Patturajan, Meera
Rieger, Daniel
Spytek, Kimberly
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Taupier Jr., Raymond
Zerhusen, Bryan
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milarity 95.0%;
Conservative
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Zhong, Mei
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Mezes, Peter
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Sequence 39, Application US/10262445
Publication No. US20040014058A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John
APPLICANT: Burgess, Catherine
APPLICANT: Catterton, Elina
APPLICANT: Chant, John
APPLICANT: Chant, John
APPLICANT: Chandhuri, Amirabha
APPLICANT: Edinger, Shlomit
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US-10-262-445-39
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Matches 1145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 749
LENGTH: 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteix
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                       OTHER INFORMATION: n e
NAME/KEY: SITE
LOCATION: (774)
OTHER INFORMATION: n e
NAME/KEY: SITE
LOCATION: (777)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prior application data removed
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: SITE LOCATION: (511.
                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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APPLICANT: FANGER, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILLING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FASTSEQ FOR Windows Version 3.0
SEQ ID NO 347
LENGTH: 1740
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Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
Wang, Aljun
Skeiky, Yasir A.W.
Henderson, Robert A.
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APPLICANT: Kalos, Michael D.
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
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CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 347
LENGTH: 1740
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; TYPE: DNA
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Pred. No. 1e-179;
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RESULT 12
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Sequence 347, Application US/09897778
; Patent No. US20020147143A1
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APPLICANT: Wang, Tongtong

APPLICANT: Marnerakis, Margarita

APPLICANT: Fanger, Gary R.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Henderson, Robert A.

APPLICANT: Henderson, Robert A.

APPLICANT: Peckham, David W.

APPLICANT: Fanger, Neil

ITITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILLE REFERENCE: 210121.455C16

CURRENT APPLICATION NUMBER: US/09/897,778

CURRENT FILING DATE: 2001-06-28

NUMBER OF SEQ ID NOS: 467

SOFTWARE: FASSESQ for Windows Version 4.0

SEQ ID NO 347

LENGTH: 1740
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; ORGANISM: Homo
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CURRENT FILING DATE: 2001-11-30
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 347
LENGTH: 1740
TYPE: DNA
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Publication No. US20030064947A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
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Best Local Similarity 64.9
Matches 1116; Conservative
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APPLICANT:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C17
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Li, Samual X.
Kalos, Michael D.
Kalos, Michael D.
Henderson, Robert #
McNeill, Patricia I
Fanger, Neil
Retter, Marca
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Fanger, Gary R.
Vedvick, Thomas S.
Carter, Darrick
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Peckman, David W.
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GGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCAGGGAAATTGTACAACAGGTG
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APPLICANT: Spies, Gregory A.

APPLICANT: Fan, Liqun

APPLICANT: Fan, Liqun

APPLICANT: Wang, Tongtong

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C18

CURRENT APPLICATION NUMBER: US/10/117,982

CURRENT FILING DATE: 2002-04-05

INUMBER OF SEQ ID NOS: 484

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 347

LENGTH: 1740

TYPE: DNA

ORGANISM: Homo sapiens

US-10-117-982-347
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US-10-117-982-347
; Sequence 347, Application US/10117982
; Publication No. US20030138438A1
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APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thoma.
APPLICANT: Carter, Darric.
APPLICANT: Watanabe, Yosh.
APPLICANT: Henderson, Rob.
APPLICANT: Kalos, Michael
APPLICANT: Kalos, Gregory
APPLICANT: Spies, Gregory
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
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Best Local Similarity 64.9%;
Matches 1116; Conservative
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                         GGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGATGAAGAGGTGAGC 552
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Vedvick, Thomas
Carter, Darrick
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Kalos, Michael D.
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Henderson, Robert A
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Pred. No. 1e-179;
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GTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTCAGAATTATC
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RESULT 15
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TYPE: DNA
ORGANISM: Homo sapiens
US-10-117-982-478
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 478
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Best Local Similarity 64.9%;
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APPLICANT: Kalos, Michael D.
APPLICANT: Mericle, Barbara
APPLICANT: Spies, Gregory A.
APPLICANT: Spies, Gregory A.
APPLICANT: Fan, Liqun
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C18
CURRENT APPLICATION NUMBER: US/10/117,982
CURRENT FILLING DATE: 2002-04-05
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Fanger, Gary R.
Vedvick, Thomas S.
Carter, Darrick
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Search completed: July 24, 2004, 22:29:09 Job time: 1427.28 secs

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ALIGNMENTS

JOURNAL MEDLINE PUBMED REFERENCE REFERENCE AUTHORS TITLE SOURCE ORGANISM ACCESSION VERSION RESULT 1 AK049196 KEYWORDS DEFINITION Locus JOURNAL MEDLINE PUBMED TITLE AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new (Genome Res. 10 (10), 1617-1630 (2000) AKO49196 3592 bp mRNA linear HTC 20-SEP-2003 Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone: C330012H03 product: HEPATOCELLULAR CARCINOMA AUTOANTIGEN homolog [Homo sapiens], full insert sequence. Genome Res. 20499374 Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999) Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Mus musculus Mus musculus (house mouse) AK049196.1 GI:26093366 HTC; CAP trapper. AK049196 11042159 10349636 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus cDNAs to genes

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P. Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Myazaki, A., Nurata, M., Koya, S., Kurihara, C., Matsuyama, T., Myazaki, R., Ohno, M., Ohsato, N., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Okazaki, Y., Saito, R., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Nuramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resægsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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6 (bases 1 to 3592)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                     prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P. Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Oho, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Genome Res. 10 (10), 1617-1630
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Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoham Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaiia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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2
Carninci, P.,
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                                                                                                               High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                      Carninci, P. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, UKL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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6 (bases 1 to 2964)
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Please visit our web site for further details
                                                                                                                                                                                                                                                                                                                                                                                        prepare mouse tissues.
Tissues were provided by Dr. Tomohiro Kono (Department of Animal
Science, Tokyo University of Agriculture, 1737 Hunako Atsugi City,
Kanagawa Prefecture, Japan) whose assistance we gratefully
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URL:http://fantom.gsc.riken.go.jp/
                                                                                                                                                                              /organism="Mus musculus"
/mol_type="mRNA"
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/strain="C57BL/6J"
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/db_xref="FANTOM_DB:B130017M24"
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/db_xref="taxon:10090"
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                     /tissue_type="parthenogenote"
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QY 2033 ICCCACGACGETATICCTTTTGTTGACATAGGTGAACGTGTTCAAAGCAAAG	1975 CAGGGCTTCTGCAGGCTTCAGCCATCCACTTCACCACTCACTTCGGATCTCTCGAAC	1917	1857 1743	QY 1798 GAATGAGACCAAACGCAGCCAGCCAGATCGGGAGCAAAGACCAT-CTGAGGAATG 1856	OY 1738 TGAGGCTCCCACAGCACCAGCAAACCAGATGAATGTAGCCCTTCCAACACCTGACA 1797	OY 1678 CAACAGGTGAAGCAGCAGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAAG 1737	QY 1618 AGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCAGGGAAATTGTA 1677	1558 1449	1498 1389	1438 1329	QY 1378 GGGCCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAAGAGGA 1437	OY 1318 TCTATCAAGATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCATCATCATCACC 1377	OY 1258 GGCGCCATCATCGGGAACAAGGGGGCACATCAAACAGCTGGCGAGATTCGCCGGAGCC 1317	1198	1141 1029	Qy 1141 1140	Db 909 GCCAATCTGATCCCAGGGCTAAACCTCAGTGCACTTGGCATCTTTTCGACTGGACTGTCT 968

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
plate: LLAM12753 row: a column: 23
High quality sequence stop: 679.
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Tissue Procurement: ATCC
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/clone lib="NH1 MGC 88"
/clone lib="NH1 MGC 88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site_1: Not1; Site_2: Sal1; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NHH_MGC Library."
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/tissue_type="duodenal adenocarcinoma,
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                                                                                                                                cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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1. (bases 1 to 874)
                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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AGENCOURT_8034698 NIH_MGC_110
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6207026"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_110"
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AACTGGGTTTTTTGCATACTG
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Similarity
                                                                                                                 /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
25.7%;
99.4%;
                               DB 13;
                           Length
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1695 GGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCAGGAAGTGAGGCTCCCACAGGCA A--CTGGTTTTTTGCATACTG TGTCACTCCTCATGCCTGTCTAGCTCATACACCCCATTTCTCTTTTGCTTCACAGGTTTTAA AGTTCTGGATCACCTGTGTATGTCAACAGAAGGGATACCGTCTCCTTGAAGAGGAAACTC TTGAGGCCACCCGCACAAAATTCACCCAGAGGGAAATCTCGTCGGAAGGACACTCACGGC TTGAGGCCACCCGCACAAAATTCACCCAGAGGGAAATCTCGTCGGAAGGACACTCACGGC GGCTTTTCTAGACTTTAAAGAATAAAGTCTTTGGGAGGTCTCACGGTGTAGAGAGGAGGAGCT GCAAATCGTCTGTACATGTGTGTACATATTAGAAAGGGAAGATGTTAAGATATGTGGC GCCAGCCAGATCGGGAGCAAACCAAAGACCATCTGAGGAATGAGAAGTCTGCGGAGGCGG CTGTGGGTTACACAGGGTGCCTGCAGCGGTAATATATTTTAGAAATAATATATCAAATAA GCAAATCGTCTCTGTACATGTGTACATATTAGAAAGGGAAGATGTTAAGATATGTGGC GTTGAACTAACATAGGTGAACGTGTTCAAAGCCAAGCAAAATGCACACCCTTTTTCTGTG GTTGAACTAACATAGGTGAACGTGTTCAAAGCCAAGCAAAATGCACACCCTTTTTCTGTG GCCATCCACTTCACCATCCACTCGGATCTCTCCTGAACTCCCACGACGCTATCCCTTTTA GCCATCCACTTCACCATCCACTCGGATCTCTCTGAACTCCCACGACGCTATCCCTTTTA CCAGGITTGCCÁGAACCÁCGAGCCCCGCCCCCCCAGGGCTTCTGCAGGCTTCA GCCAGCCAGATCGGGAGCAAACCAAAGACCATCTGAGGAATGAGAAGTCTGCGGAGGCGG CCAGCAAAACAACGGATGAATGTAGCCCTTCCAACACCTGACAGAATGAGACCAAACGCA 181 GGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAGTGAGGCTCCCACAGGCA CCAGCAAAACAACGGATGAATGTAGCCCTTCCAACACCTGACAGAATGAGACCAAACGCA Conservative 0, Score 842.2; DB 13; Pred. No. 2.3e-154; 0; Mismatches 3; 2553 Indels 2 Gaps 2534 2474 2114 1994 2414 2354 2294 2234 2174 780 720 660 600 540 360 2054 300 1934 480 420 1874 120 240 180 60 1754 بر ..

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AGENCOURT_7559207 NIH_MGC_72
5', mRNA sequence.
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Tissue Procurement: ATCC/DCTD/DTP
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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/lab_host="DH10B (phage-resistant)"
/clone lib="WIH MGC 72"
/note="Organ: Skin; Vector: pCMV-SPORT6;
Site_2: Sall; Cloned unidirectionally. P
Average insert size 2 kb. Library const
Technologies."
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Homo sapiens cDNA clone IMAGE:6046477
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Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, Fobo, G., Han, M. and Wiemann, S. EST (Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DKFZp781G0234_r1 781 (synonym: DKFZp781G0234_5', mRNA sequenc
                                                                                                            No s1 sequence available. This clone (DKFZp781G0234) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                       Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Research Center (DKPZ); Email s.wiemann@dkfz-heidelberg. sequenced by Qiagen (Hilden/Germany) within the cDNA sequencentum of the German Genome Project.
                                                                                                                                                                                                                                                                                                          Contact: MIPS
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                                                /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                          /organism="Homo
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/note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Comporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13368 row: n column: 02
High quality sequence stop: 670.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, I
Unpublished (1999)
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Mammalia; Eutheria;
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                                                                                     CTTGAAGAGAAACTCTGTCACTCCTCATGCCTGTCTAGCTCATACACCCCATTTCTCTTT
                                                                                                                                                                     GAAGGACACTCACGGCAGTTCTGGATCACCTGTGTATGTCAACAGAAGGGATACCGTCTC
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NH1 MGC_72"
/note="Organ: skin; Vector: pCMV-spORT6; Site_1:
Site_2: Sall; Cloned unidirectionally. Primer:
Average insert size 2 kb. Library constructed
Technologies."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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0; Mismatches 9;
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    261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image-llnl.gov
plate: LLAM12276 row: c column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1089)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
                                                                                                                                             Conservative
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/lab host="DH10B (phage-resistant)"
/clome_lb="NIH_MGC_71"
/clome_tb="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
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AGENCOURT 7965128 NIH_MGC_72
5', mRNA sequence.
BU156245
                                                                           Homo sapiens
Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 894)
                                                                                                                                 EST
                                                                                                                                                         BU156245.1 GI:22669777
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National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                          CTCTTTGCTTCACAGGTTTTAAACTGGTTTTTTGCATACTGCTATATAATTCTCTGTGTCTC
                                                                                       CGTCTCCTTGAAGAGGAAACTCTGTCACTCCTCATGCCTGTCTAGCTCATACACCCATTT
                                                                                                                                                        TCGTCGGAAGGACACTCACGGCAGTTCTGGATCACCTGTGTATGTCAACAGAAGGGATAC
CTCTTTGCTTCACAGGGTTTAAACTGGTTTTTTGCATACTGCTATATAATTCTCTGTCTC
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//lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo of Average insert size 2 kb. Library constructed by Life Technologies."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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NIH-MGC http://mgc.nci.nih.gov/
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Unpublished (1999)
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                                                                                                        Conservative
                                                                                                                                                                                  /tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="NHH MGC 87"
/clone lib="NHH MGC 87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NHH_MGC Library."
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Pred. No. 8.3e-137;
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AGENCOURT 14121251 NIH MGC 180 Homo
IMAGE:30383283 5', mRNA sequence.
CD243351
                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Butheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 940)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
                                                                                                                                                                                       CD243351
CD243351.1
Email: cgapbs-r@mail.nih.gov
Tissus Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                               Unpublished (1999)
                                                     Contact: Robert Strausberg, Ph.D.
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High quality sequence stop: 695.
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                                              rcacraagcagacccagrcccgggragararccaragaaaagagaacrcrggagcrgcag
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/clone lib="NIH MGC_180"
/clone lib="NIH MGC_180"
/note="Organ: Testis; Vector: pCMV-SPORT6.1; Site_1: Not1;
Site_2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.68 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC
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Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) wit
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AGENCOURT 15622249 NIH MGC 147 Homo
IMAGE:30531076 5', mRNA sequence.
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                                                                                                     GGCAGCGGAGGAGGAGCGACGAGCGCCGGGTACCGGGCCCGGGGGAGCCGCGGGCCTCTCGGGG
                                AAGAGACGGATGATGAACAAGCTTTACATCGGGAACCTGAGCCCGGCCGTCACCGCCGAC 120
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31 Rm10A07 Bethesda, MD 20892
                                                                                                                                                                                                                                                     /clone_lib="NIH_MGC_147"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
all-XhoI; Site_2: BamH; Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: This
a NIH_MGC library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:30531076"
/tissue_type="Human Placenta"
/lab_host="DH10B TonA"
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Pred. No. 2.9e-136;
0; Mismatches 3;
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            DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1677 row: c column: 02
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                               602705902F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4842553
                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
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sequence stop:
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TGTCACCATCCATGCCACCCCAGAGGGGACTTCTGAA--GCATGCCGCATGATTCTTGAA
                                                                    GCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCTGGAGCTGCAGAGAAAGCC
                                                                                                                                        CACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGAACATCACTAA
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                                                                                                                                                                                                        CGCCCTGGGGGCACTTCTCAGGCCAGACAGATTGATTTCCCGGCTGCGGATCCTGGTCCC
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/clone="IMAGE:4842553"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 43"
/clone lib="NIH MGC 43"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
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Pred. No. 1.6e-135;
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Query Match
Best Local Similarity
Matches 731; Conserv
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AGENCOURT 10049220 NIH MGC 142 Homo
IMAGE:6495584 5', mRNA sequence.
BU601634
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7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 762)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                          GGCAGCGGAGGAGGAGGAGGAGCGCCGGGGTACCGGGGCCGGGGGAGCCGCGGGCTCTCCGGGG
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / LINE LINE 1933 | The content of the NAS | "
/ tissue type="mixed (pool of 40 RNAS)"
/ lab host="DH10B (T1-phage-resistant)"
/ clone lib="NIH MGC 142"
/ clone lib="NIH MGC 1
                                                                                                                                                                                                                                                                                                                                                                                                                    5'-ATTCTAGAGGCCGAGCAGGCCGACATG-dT (30) NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the >0.5 kb size fraction (other fractions present in NIH MGC 141). Library created in the laboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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/db_xref="taxon:9606"
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99.6%;
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                                                                                                                                                                                    0;
                                                                                                                                                                                         Score 718.8; DB 13; Pred. No. 3.5e-130; 0; Mismatches 2;
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AAGAGACGGATGATGAACAAGCTTTACATCGGGAACCTGAGCCCGCCGCCGTCACCGCCGAC 120

Db	8	Ф	Qy	B	γQ	Db	γQ	Ъ	Ş	Db	γQ	В	γQ	Db	γQ	Db	Ş	DЪ	Qy	Db	8
727 GAACATCACTAAGC 740	720 GAACATCACTAAGC 733	667 GATCCTGGTCCCCACCAGTTTGTTGGTGCCATCGGAAAGGAGGGCTTGACCATAAA 726	660 GATCCTGGTCCCCACCCAGTTTGTTGGTGCCATCATCAGAAAGGAGGGCTTGACCATAAA 719	607 GAGCAAGGCCACGCCCCTGGGGGCACTTCTCAAGCCAGACAGA	601 GAGCAAGGCCACG-CCCCTGGGGGCACTTCTCAGGCCAGACAGATTGATTTCCCGCTGCG 659	547 GAAGAGGTGAGCTCCCCTTCGCCCCCTCAGCGAGCCCAGCGTGGGGAGCCACTCTTCCCGG 606	541 GAAGAGGTGAGCTCCCCTTCGCCCCCTCAGCGAGCCCAGCGTGGGGAGCCACTCTTCCCGG 600	487 GAGAAGCTAAGCGGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGAT 546	481 GAGAAGCTAAGCGGGCATCAGTTTGAGAA	427 ACAGAAAACCGCCGTTGTCAACGTCACATATGCAACAAGAGAAGAAGCAAAAATAGCCATG 486	421 ACAGAAACCGCCGTTGTCAACGTCACATATGCAACAAGAGAAGAAGAAGAAAATAGCCATG 480	367 TTGGATGGACTTTTGGCTCAATATGGGACAGTGGAGAATGTGGGAACAAGTCAACACAGAC 426	361 TTGGATGGACTTTTGGCTCAATATGGGACAGTGGAGGAACGAGACAAGTCAACACAGAC 420	307 AAGCTAAGGAAGATTCAGATTCGAAACATCCCTCCTCACCTGCAGTGGGAGGTG 366	301 AAGCTAAGGAGCAGGAAAATTCAGATTCGAAACATCCCTCCTCACCTGCAGTGGGAGGTG 360	247 CTCTCGGGTAAAGTGGAAATTGCATGGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAA 306	241 CTCTCGGGTAAAGTGGAATTGCATGGGAAATCATGGAAGTTGATTACTCAGTCTCTAAA 300	187 TCCGGCTACGCCTTCGTGGACTACCCCGACCAGAACTGGGCCATCCGCGCCATCGAGACC 246	181 TCCGGCTACGCCTTCGTGGACTACCCCGACCAGAACTGGGCCATCCGCGCCCATCGAGACC 240	127 GACCTCCGGCAGCTCTTTGGGGACAGGAAGCTGCCCCTGGGCGGACAGGTCCTGCTGAAG 186	/ 121 GACCTCCGGCAGCTCTTTGGGGACAGGAAGCTGCCCCTGGCGGGACAGGTCCTGCTGAAG 180

Search completed: July 24, 2004, 16:42:45 Job time: 8228.67 secs

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Result
No.
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-MODEL-frame+ n2p.model -DEV=xlp
-MODEL-frame+ n2p.model -DEV=xlp
-Q-/cgn2 1/USFTO_Spool p/US09270437/runat_23072004 095738 27403/app query.fasta_1.5582
-DB=A Geneseq 29Jan04 -OPMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pot -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLIN=2000000000
-USER=US09270437 @GGN 1 1 185 @runat 23072004 095738 27403 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQÜERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: geneseqD1980s:*
2: geneseqD1990s:*
3: geneseqD2000s:*
4: geneseqD2001s:*
5: geneseqD2002s:*
6: geneseqD2003bs:*
7: geneseqD2003bs:*
8: geneseqD2004s:*
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Ygapop 10.0 , )
Fgapop 6.0 , I
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Copyright (c) 1993 - 2004 Compugen Ltd
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Human lun
Human lun
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

11 1875 31.9 579 5 ABB7554 12 1875 31.9 579 5 ABB7554 13 1875 31.9 579 5 ABB7554 14 1875 31.9 579 7 ADB2317 14 1875 31.9 579 7 ADB2317 15 1875 31.9 579 7 ADB2317 16 1875 31.9 579 7 ADB2318 17 1875 31.9 589 7 ADB2318 18 1870 31.8 586 5 ABB75194 18 18 18 18 18 18 18 18 18 18 18 18 18 1	OXFXERXAXHXEE	XXXXXXXXX	M M D X D X F X	
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The invention relates to isolated polynucleotide (I) and polypeptide (II) creation (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed conditions of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal consecutivity of (II) or to treat disease states involving (II). (II) is considered in tissue, as molecular weight markers and as a food considered expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating an involving aberrant proceed expression or hological activity. The colving aberrant proceed expression or hological activity. The colving aberrant proceed mapping, identification of mutations in constitution of genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and camino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in celectronic format directly from WIPO at fixed the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the
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the expression level of a marker in a patient sample and the normal level of expression of the marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing ovarian cancer (e.g. patients having a familial history of ovarian cancer). The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzheimer's disease or Parkinson's disease), brain inflammations (e.g. bacterial or viral meningitis or encenhalistics),
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                                                                                                                                                                                                                                                                                                                                                                                                 The present invention patient is afflicted
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Morrisey MP, Olandt PJ, Sen A,
u K, Schmandt RE, Zhao X, Glatt
                                                                                                                                                                                                                                                                                                                                                                                           invention relates to a new method afflicted with ovarian cancer. The
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Best Local Similarity:
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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WO200175067-A2

11-OCT-2001

30-MAR-2001; 2001WO-US008631

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

(HYSE-) HYSEQ INC.

RT, Liu ū ΥŢ;

WPI: 2001-639362/73.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 20; SEQ ID NO 37153; 103pp; English.

control of the first transformers of the first transformers. (I) is useful as hybridisation probes, polymerase chain condition (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed activity of (II) or to treat disease states involving (II). (II) is considered in tissue, as molecular weight markers and as a food golypeptide in tissue, as molecular weight markers and as a food golypeptide in tissue, as molecular weight markers and as a food of sites expressing (II). (I) and (II) are useful in medical imaging convolving aberrant protein expression or biological activity. The colypeptide and polynucleotide sequences have applications in colypeptide and polynucleotide sequences have applications in colypeptide and polynucleotide sequences have applications in colypeptide and polynucleotide sequences have applications in colypeptide and polynucleotide sequences have applications in colypeptide and polynucleotide sequences have applications in colypeptide and polynucleotide sequences have applications in colypeptide and polynucleotide sequences have applications in colypeptide and polynucleotide sequences have applications in colypeptide and polynucleotide sequences have application of mutations colypeptide colypeptide in types of data and products dependent on DNA and colypeptide in the printed specification, but was obtained in celectronic format directly from WIPO at colypeptide in the printed specification, but was obtained in the printed specification, but was obtained in celectronic format directly from WIPO at The invention relates to isolated polynucleotide (I) and polypeptide polymerase chain

Sequence 614

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Best Local Similarity:
Query Match:
                                            Alignment
                      Percent Similarity:
                              Score:
                                     No.:
                                             Scores:
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92.05%
92.05%
48.19%
Gaps:
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Matches:
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US-09-270-437D-8 (1-3283) x ABG06794 (1-614)

Db 4	Oy 14	Db 2	Ογ 8:	מם	Qy 2:	
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                                         {\tt lyLeuAsnLeuSerAlaLeuGlyIlePheSerThrGlyLeuSerValLeuSerProProA}
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	493 GGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGATGAAGAGGTGAGC 552 	433 GTTGTCAACGTCACATATGCAACAAGAAGAAGAAGCAAAAATAGCCATGGAGAAGCTAAGC 492 	373 TTGGCTCAATATGGGACAGTGGAGAATGTGGAACAAGTCAACAGACAG	313 AGGAAAATTCAGATTCGAAACATCCCTCCTCACCTGCAGTGGGAGGTGTTGGATGGA	253 GTGGAATTGCATGGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAGCTAAGGAGC 312 	193 TTCGTGGACTACCCCGACCAGAACTGGGCCATCCGCGCCATCGAGACCCTCTCGGGGTAAA 252 	133 CTCTTTGGGGACAGGAAGCTGCCCCTGGCGGGACAGGTCCTGCTGAAGTCCCGGCTACGGC 192 	73 ATGAACAAGCTTTACATCGGGAACCTGAGCCCCGCGTCACCGCCGACCGA	22 CGCCGGGTACCGGGCCGGGGGAAGAAGAGACGGATG 72 3 ArgArgTyrAlaCysArgTyrArgSerGlyIleProGlySerThrHisAlaSerGlyMet 22	-270-437D-8 (1-3283) x AAU16163 (1-620)	t Similarity: 90.78% Conservative: ocal Similarity: 90.61% Mismatches: 47.71% Indels: 49.51%	ment Scores: No.: 6.82e-252	components. The inverse part of the popular to the	regenerate tissues and in Chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins,	can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to	arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, cerevous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the coordination of the content of th	immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (BIISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the hreast or liver and immunity and include autoimmune.	pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and is discover.	encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
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Created disorders (e.g. theart of sources (e.g. Abu55748 represent human novel polypeptides and their associated CC polynucleotides. The polypeptides and polynucleotides are useful in gene CC therapy for treating, inhibiting or preventing neural disorders, immune CC and multiple sclerosis), muscular disorders, repriatory diseases (e.g. CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g. CC gastrointestinal disorders, pulmonary disorders, reproductive disorders (c.g. congenital heart defects, Ebstein's anomaly and hypoplastic left (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left (c.g. theart syndrome), renal disorders (e.g. acute kidney failure and end-stage (c.g. appendicitis), allergic reactions and conditions (e.g. asthma), blood crelated disorders (e.g. thrombosis, atherosclerosis and myocardial (c.g. appendicitis), allergic reactions and conditions (e.g. asthma), blood crelated disorders (e.g. thrombosis, atherosclerosis and myocardial (c.g. ABU55748 represent human novel polypeptides of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alsobrook JP, Burgess CE, Catterton E, Chant JS, Chan Eddinger SR, Gerlach VL, Giot L, Gorman L, Guo X, Kel Mezes PS, Millet I, Ooi CE, Patturajan M, Rieger DK, Taupier RJ, Zerhusen BD, Zhong H, Zhong M;
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N-PSDB; AAZ10617.
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                                            AlaileileGlyLysLysGlyGlnHisileLysGlnLeuSerArgPheAlaSerAlaSer
                                                                        GCCATCATCGGGAAGAAGGGGGCACACATCAAACAGCTGGCGAGATTCGCCGGAGCCTCT
                                                                                                       PheMetGlnAlaProGluGlnGluMetValGlnValPheIleProAlaGlnAlaValGly
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                                                                                                                                                                                             ---TCCAGCCTGTACCCCCATCACCAG
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17-DEC-1999;
30-DEC-1999;
10-JAN-2000;
This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polymucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the
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                                                                            Claim
                                                                                                       Isolated polypeptide comprising an immunogenic portion of a protein is used for detecting and monitoring progression of
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US-09-270-437D-8 (1-3283) x AAB11365
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Query Match:
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                                         GCAGAGAAGCCTGTCACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATG
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ATTCTTGAAATCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTG
                          AlaGluLysSerIleThrIleLeuSerThrProGluGlyThrSerAlaAlaCysLysSer
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ID ABB7
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                lung cancer; cytostatic;
                                    recombinant protein sequence SEQ ID NO:446.
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2000US-00630940.
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                                ng A, Skei
Fanger N,
Carter D,
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                              Skeiky YAW, Li S
er N, Retter MW,
er D, Watanabe Y,
                                SX, Kalos MD,
, Marnerakis M,
Y, Peckham DW;
                                         Henderson
Fanger GR
                                            요.
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Polynucleotides encoding lung cancer or stimulating ng an tumor polypeptides,
immune response. useful for treating

Claim 2; Page 365-367; 374pp; English

tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present The present invention describes human lung tumour proteins. Human lung fusion

Sequence 579 AA,

Percent Similarity: Best Local Similarity: Match: No 5.47e-165 1875.00 78.70% 64.96% 31.86% Length: Matches: Conservative: Gaps: Mismatches: Indels: 579 369 78 95 26

US-09-270-437D-8 (1-3283) x ABB75053 (1-579)

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                                   ArgLysLeuGlnIleArgAsnIleProProHisLeuGlnTrpGluValLeuAspSerLeu
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CCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAAGAGAAAAC
                                        ATCAAGATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCATCACCGGG
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                                                                                                                                               PheGluGln---SerGluThrGluThrValHisLeuPheIleProAlaLeuSerValGly
                                                                                                                                                                CATCACTCTTATCCAGAGCAGGAGATTGTGAATCTCTTCATCCCAACCCAGGCTGTGGGC
                                                                                                                                                                                                 {\tt SerGlyMetProProProThrSerGlyProProSerAlaMetThrProProTyrProGln}
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The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present

Example 2; Page 330-332; 374pp;

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15-SEP-2000; 2000US-00662786.
09-OCT-2000; 2000US-00685696.
12-DEC-2000; 2000US-00735705.
07-MAY-2001; 2001US-00850716.
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09-OCT-2000;
12-DEC-2000;
07-MAY-2001;
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   TTCTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACA 1500
                     ProProGluAlaGinPheLysAlaGinGlyArglieTyrGlyLysIleLysGluGluAsn
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CC The present invention describes isolated human lung carcinoma
CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
CC activity, and can be used in gene therapy and in vaccines. Compositions
CC comprising (I) or (II) can be used for stimulating an immune response in
CC (I) can be used for treating lung cancer in a patient. Oligonucleotides of
CC (I) can be used for detecting the presence of a cancer in a patient, by
CC obtaining a biological sample from the patient, contacting the biological
CC sample with the oligonucleotide, detecting in the sample, an amount of
CC polynucleotide that hybridises to the oligonucleotide and comparing the
CC amount of polynucleotide that hybridises to the oligonucleotide to a
CC the patient. (I) and (II) are useful in pharmaceutical compositions, e.g.
CC vaccines. (I) is useful as a marker to indicate the presence or absence
CC of a cancer such as lung cancer. ABQ92145 to ABQ9286 and ABP61866 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-DEC-2000;
07-MAY-2001;
28-JUN-2001;
                                                                                                                                                                                                                                                              Novel lung carcinoma polynucleotide sequences and polypeptides encoded the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer.
                                                                                                                                                                                                                                           Example
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Watanabe Y,
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                                                                  ATTCTTGAAATCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTG
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                                         AlaGluLysSerTleThrileLeuSerThrProGluGlyThrSerAlaAlaCysLysSer
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RESULT 13
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                                                                                                        07-OCT-2002
                                                                                                                              ABP61974;
              WO200247534-A2
                                   Homo sapiens
                                                       Human; lung cancer;
                                                                               Human lung cancer associated protein sequence
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                                                                                                                                                     protein;
                                                          lung tumour; cytostatic; gene therapy; vaccine
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                                                                                   SEQ ID NO:449
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The present invention describes isolated human lung carcinoma CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic CC comprising (I) or (II) can be used in gene therapy and in vaccines. Compositions CC comprising (I) or (II) can be used for stimulating an immune response in CC a patient and for treating lung cancer in a patient. Oligonucleotides of CC a patient and for treating lung cancer in a patient. Oligonucleotides of CC sample with the oligonucleotide, detecting the patient, by CC (I) can be used for detecting the patient, contacting the biological CC sample with the oligonucleotide, detecting in the sample, an amount of CC amount of polynucleotide that hybridises to the oligonucleotide to a CC concentrate of the cut-off value, and determining the presence of a cancer in CC the patient. (I) and (II) are useful in pharmaceutical compositions, e.g. CC vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABQ92145 to ABQ92486 and ABP61866 to CC ABP61992 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang T,
Mcneill
                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel lung carcinoma polynucleotide sequences and polypeptides encoded the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer.
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07-MAY-2001; 2001US-00850716.
28-JUN-2001; 2001US-00897778.
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                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; Page 375-377; 381pp; English.
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Sequence 579
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Watanabe Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y YAW, Li SX, Kalos MD, Henderson
Retter MW, Durham M, Fanger GR, V
Peckham DW, Cai F, Foy TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vedvick TS;
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Percent Similarity:
Best Local Similarity:
Query Match: Score: Pred. No.:

Scores: 5.47e-165 1875.00 78.70% 64.96% 31.86%

Alignment

Length:
Matches:
Conservative: Mismatches: Indels:

369 369 78 26

US-09-270-437D-8 (1-3283) x ABP61974 (1-579)

Db

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δÃ 당 Ş dq 100

Ś B Š 뮍 Ś 밁 8 뭥 В S 193 253 61 21 73 81 CTCTTTGGGGACAGGAAGCTGCCCCTGGCGGACAGGTCCTGCTGAAGTCCGGCTACGCC MetAsnLysLeuTyrIleGlyAsnLeuSerGluAsnAlaAlaProSerAspLeuGluSer ATGAACAAGCTTTACATCGGGAACCTGAGCCCGCCGTCACCGCCGACGACCTCCGGCAG TTCGTGGACTACCCCGGACCAGAACTGGGGCCATCCGGGCCATCGAGACCCTCTCGGGTAAA TTGGCTCAATATGGGACAGTGGAGAATGTGGAACAAGTCAACACAGACACAGAAACCGCC 80 60 40 192

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                                                                                                                                                                                                                                                                                                                         Human lung cancer
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DB; ABQ92483.
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PD, Fanger N,
), Watanabe Y,
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er N, Retter MW, Durham M, Fanger GR,
be Y, Peckham DW, Cai F, Foy TM;
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Novel lung carcinoma polynucleotide sequences and polypeptides e the polynucleotides, useful in pharmaceutical compositions such vaccines and as markers to indicate the presence of lung cancer.

Claim 9; Page 372-374; 381pp; English.

The present invention describes isolated human lung carcinoma polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the oligonucleotide to a predetermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions, e.g.

8 멂 S 밁 Ś В Ş 당 γQ 뮍 8 뮰 8

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                     CATCACTCTTATCCAGAGCAGGAGATTGTGAATCTCTTCATCCCAACCCAGGCTGTGGGC
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GlnValLysGlnHisGlnGlnGln
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21-AUG-2000;
15-SEP-2000;
09-OCT-2000;
12-DEC-2000;
07-MAY-2001;
28-JUN-2001;
                                                                                                                                                                                                                                                                                                                The invention describes isolated polynucleotides and polypeptides useful for diagnosing, preventing and/or treating cancer, particularly lung cancer. A new isolated polynucleotide comprises: any of the 22 fully defined nucleotide sequences (e.g. 1012, 900 or 2773 bp) given in the specification; complements of the nucleotide sequences cited above; at least 10 contiguous residues of the nucleotide sequences cited above; a sequence that hybridise to any of the nucleotide sequences under highly stringent conditions; a sequence that is at least 75 or 90% identical to the above nucleotide sequences, or degenerate variants of the above nucleotide sequences. The composition and methods are useful in diagnosing, preventing and/or treating cancer, particularly lung cancer, in gene therapy and in vaccines. This is the amino acid sequence of a recombinant human lung tumour associated protein.
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27-UUL-1998;
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                             SerGlyMetProProThrSerGlyProProSerAlaMetThrProProTyrProGln
                                                                                        LeuGlnAlaHisLeuIleProGlyLeuAsnLeuAsnAlaLeuGlyLeuPheProProThr
                                                                                                                                               GluGluIleMetLysLysIleArgGluSerTyrGluAsnAspIleAlaSerMetAsn
                                                                                                                                                                                                                                                                                                                         LysIleLeuAlaHisAsnAsnPheValGlyArgLeuIleGlyLysGluGlyArgAsnLeu
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1620	1561 GCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTCAGA 1
538	:::
1560 518	1501 GCTGGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGAAC
1500	1441 TTCTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACA 1500
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1440	1381 CCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAAGAGGAAAAC 1
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-09-252-991A-2	-09-252-991A-2425	-09-252-991A-3181	-09-252-991A-2714	-09-252-991A-2542	-09-252-991A-1943	-09-252-991A-1803	-09-252-991A-2748	-09-252-991A-1776	-09-252-991A-1842	-09-252-991A-2979	-09-252-991A-294;	-08-187-793-2	-09-252-991A-3	-09-252-991A-3265	-09-261-855-1	-09-261-855-23	-09-252-991A-2800	09-252-991A	-09-252-991A-3079	-09-252-991A-2188	-09-261-855-1	-09-261-855-2	09-261-855-2	-08-187-793-4	-09-261-855-1	09-261-85	9-261-855-2	-US94-01782-	08-726-160-8	-08-021-608D-8	94-01782-	US-08-726-160-10
quence 2	equence 24254.	equence 31814	equence 27142	equence 25423.	equence 1943	equence 18035.	equence 27483,	equence 17764,	equence 18427,	e 29790.	equence 29427.	equence 2. Appl	equence 31760.	equence 32659.	equence 19, Apr	equence 23, Apr	equence 28001,	quence 24009	equence 30792.	equence 21881,	equence 17. Apr	equence 22. Apr	equence 21. Apr	equence 4. Ann	equence 18. Apr	equence 24. Apr	equence 20	quence 8.	equence 8,	quence 8	equence 10	equence 10

ALIGNMENTS

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APPLICANT: ROSS, Jeffrey
INTER OF INVENTION: THE C-MYC CODING REGION I
ITITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC
FILE REFERENCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 577
TYPE: PRT
TYPE: PRT
ORGANISM: MUS musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09261855A Patent No. 6255055
GENERAL INFORMATION:
                                   133 CTCTTTGGGGACAGGAAGCTGCCCCTGGCGGAACAGGTCCTGAAGTCCGGCTACGCC
21 ValPheAlaGluHisLysIleSerTyrSerGlyGlnPheLeuValLysSerGlyTyrAla
                                                                                                     73 ATGAACAAGCTTTACATCGGGAACCTGAGCCCCGCCGTCACCGCCGACGACCTCCGGCAG 132
                                                                   MetAsnLysLeuTyrTleGlyAsnLeuAsnGluSerValThrProAlaAspLeuGluLys
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1934.00
79.10%
65.80%
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Matches:
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                                                                                                                                                           GCTGCAGAGAAGCCTGTCACCATCCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGC
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SerSerSerAlaValProProProProSerSerValThrGlyAlaAlaProTyrSerSer
                                                                             ThrLeuTyrAsnProGluArgThrIleThrValLysGlyAlaIleGluAsnCysCysArg
                                                                                                                                AGCATATACAACCCGGAAAGAACCATCACTGTGAAGGGCAGAGTTGAGGCCTGTGCCAGT
                                                                                                                                                                                                    LeuLysIleLeuAlaHisAsnAsnPheValGlyArgLeuIleGlyLysGluGlyArgAsn
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                                       SerLeuGlnSerHisLeuIleProGlyLeuAsnLeuAlaAlaValGlyLeuPheProAla
                    -TCCAGCCTGTACCCCCATCACCAG
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APPLICANT: LI, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: HOMERILL PATTION MUTHOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG C!
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUTHER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 348
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-643-597-348
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US-09-643-597-348
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Patent No. 6426072
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Fanger, Gary R.
Li, Samuel X.
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Fan, Liqun
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-09-270-437D-8 (1-3283)

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ATATACAACCCGGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCT
                                                                                                                  LysīleLeuAlaHisAsnAsnPheValGlyArgLeuIleGlyLysGluGlyArgAsnLeu
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APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG GIFTLE REFERENCE: 210121.455CB; CURRENT APPLICATION NUMBER: US/09/542,615A; CURRENT FILING DATE: 2000-04-14
    Percent Similarity:
                    Score:
                                          Alignment Scores:
                                                                       US-09-542-615A-348
                                                                                  NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 348
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-542-615A-348
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                                 No.:
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Bangur, Chaitanya S.
Hosken, Nancy A.
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                                       LysīleLeuAlaHisAsnAsnPheValGlyArgLeuIleGlyLysGluGlyArgAsnLeu
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               APPLICANT: Wang, Aijun
APPLICANT: Skeik, Yasir A.W.
APPLICANT: Skeik, Yasir A.W.
APPLICANT: Skeik, Yasir A.W.
APPLICANT: Skeik, Yasir A.W.
APPLICANT: Skeik, Yasir A.W.
AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION UNMEER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 348
LENGTH: 579
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya
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        LENGTH:
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| GlnValLysGlnHisGlnGlnGln 566
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US-09-643-597-176
; Sequence 176, Application
; Patent No. 6426072
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  GENERAL INFORMATION:
APPLICANT: Wang, To
APPLICANT: Fan, Liq
APPLICANT: Kalos, M
APPLICANT: Bangur,
APPLICANT: Hosken,
APPLICANT: Fanger,
APPLICANT: Fanger,
APPLICANT: Wang, Ai
APPLICANT: Wang, Ai
APPLICANT: Wang, Ai
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NT: Wang, Aijun
NT: Skeiky, Yasir A.W.
NT: Skeiky, Pasir A.W.
NT: Henderson, Robert A.
NT: MCNeill, Patricia D.
F INVENTION: COMPOSITIONS J
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Kalos, Michael D.
Bangur, Chaitanya (
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAL
FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 176
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
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                                              RESULT 6
US-09-480-884A-176
                         Sequence 176, Application Patent No. 6482597 GENERAL INFORMATION:
     APPLICANT: Wang, Tongtong APPLICANT: Fan, Liqun APPLICANT: Hosken, Nancy
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Best Local Query Match DB:

Percent Similarity: Best Local Similarity:

Score:

No

US-09-480-884A-176

TYPE: PRT ORGANISM: Homo

sapiens

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; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CP.
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYDE: DET
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Sequence 176, Application Patent No. 6518256 GENERAL INFORMATION:
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APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy R.
APPLICANT: Hosken, Nancy R.
APPLICANT: Fanger, Gary R.
ITILE OF INVENTION: AND DIAGNOSIS OF LUNG CAN TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAN FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PAT
ORGANISM: Homo sapiens
US-09-542-615A-176
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; Sequence 176, Application US/09606421B
; Patent No. 6531315
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael
APPLICANT: Bangur, Chaitar
APPLICANT: Hosken, Nancy
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SOFTWARE: FASTSEQ for Windows Version
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT FILING DATE: 2000-06-28
CURRENT FILING DATE: 2000-06-28
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Fanger, Gary R.
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                                       AlaGluValValValProArgAspGlnThrProAspGluAsnAspGlnValValValLys
                                                            GCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTCAGA
                                                                                                        PheValSerProLysGluGluValLysLeuGluAlaHisIleArgValProSerPheAla 498
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                                                        US-09-270-437D-8 (1-3283) x US-08-021-608D-2 (1-644)
                                                                                    Query Match:
DB:
                                                                                                            Best Local Similarity:
                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                             US-08-021-608D-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application Patent No. 5580760
                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNAY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 22-FEB-CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                           MOLECULE TYPE: PE
                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                        No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                            rGlyProProAspArgCysGlnHisAlaAlaGluIleIleThrAspLeuLeuArgSerVa 346
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                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
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APPLICANT:
                                                                                                                 APPLICATION NUMBER: FILING DATE: 04-007
                                                                                                                                                                                                                                                                                                                                                            CITY: NEW YORK STATE: NEW YORK
       CLASSIFICATION:
                             APPLICATION NUMBER: FILING DATE: 22-FE
                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                       UMBER: US/08/726,160
04-OCT-1996
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
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NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,
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STRANDEDNESS: Sin
TOPOLOGY: Unknown
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1803 AGACCAAACGCAGCCAGATCGGGAGCAAACCAAAGACCATCTGAGGAATGAGAAGT 1862	1743 CTCCCACAGCAAAACAACGGATGAATGTAGCCCTTCCAACACCTGACAAGAATG 1802 1743 1yProProGly-ProGly	1633TTCTTTGCTAGCCAGACTGCACAGGCGCAAGATCAGGGAAATTGTACAACA 1682 ::: :::	393 yLysGlyGluThrIleLysSerIleSerGlnGlnSerGlyAlaArgIleGluLeuGL 413 1578 TCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTCAGAATTATCGGGCAC 1632 1678 1679 1779 1779 1779 1779 1779 1779 1779			1408 1425 	1377 CGGGCCACCGGAAGCCCAGTTCAAGGCCCAG 1407 	1317 CTCTATCAAGATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCAC 1376	gggcgc 1GlyIl	GCATCATCA	1137 TAACACCCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGTTTGGCCCGTTCCC 1196	1077 TGCTGAGATAGAGATTATGAAGAAGCTGCGTGAGGCCTTTGAAAATGATATGCTGGCTG		972 ACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATATACAACCC 1031 972 ACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATATACAACCC 1031 972 ACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATATACAACCC 1031 972 ACATGAAACAGGGACCAAGACCAACATTTGCAGATTTGAGCATTACAACCC 1031 972 ACATGAAACAGGGACCAAGACCAACATTTGCAGATTTGAGCATTACAACCC 1031 972 ACATGAAACAGGACCAAGACCAACACAACACAACACAAC	912 ACACAATGGCTTGGTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTGAAGAAAATTTGA 971
Alignment Scores: 1.52e-14 Length: 644 Pred. No.: 263.50 Matches: 140 Score: 263.50 Conservative: 86	; FEATURE: ; NAME/KEY: ; LOCATION: ; LOCATION: ; IDENTIFICATION METHOD: ; OTHER INFORMATION: ; OTHER INFORMATION: Amino Acid 149 (Xaa) is Met or Ile pcT-US94-01782-2	HAPLOTYPE: ; TISSUE TYPE: ; CELL TYPE: ; CELL LINE: HL60 ; ORGANELLE:	AH HO	LENGTH: 644 ; TYPE: Amino Acid ; TYPE: Amino Acid ; STRANDEDNESS: Single ; TOPOLOGY: Unknown ; MOLECULE TYPE: Peptide/Protein	TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 758-4800 TELEPAX: (212) 751-6849 INFORMATION FOR SEQ ID NO: 2: GEOTENCE CHARACTERISTICS:	ATTORNEY/AGENT INFORMATION: NAME: WILLIAM S. FEILER REGISTRATION NUMBER: 26,728 REFERENCE/DOCKET NUMBER: 2026-4063PCT	ZHO	SOFTWARE: WORDDERFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/01782 FILING DATE: 22-FEB-1994	COMPUTER READABLE FORM: MEDIUM TYPE: FLORY DISK COMPUTER: IBM PC COMPATIBLE COMPATING SYSTEM: PC-DOS/MS-DOS	NEW YO	NUMBER OF SEQUENCES: 10 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: MORGAN & FINNEGAN ; STREET: 345 PARK AVENUE	AS HEA NVENT	01782-2 e 2, App L INFORM	1920 GGCGGGGAGAGCLAGGLAGGLAGGLAGGLAGGLAGGLAGG	494

Db 226 GHARACC	136 eAlaProAspSerGlyĠİyLe 816 GGGGACTTCTGAAGCATGCCGCATG 816 GGGGACTTCTGAAGCATGCCGCATG 1	516 CT 59 yT 576 CQ 79 aP 636 CAC 636 CQC 116 eGI 116 eGI	set Local Si lery Match: 1: -09-270-4371 10 10 396 23 456
US-08-021-608D-10 Sequence 10, Application US/08021608D Patent No. 5580760 GENERAL INFORMATION: APPLICANT: LEVENS, DAVID L., DUNCAN, APPLICANT: ROBERT C., AND AVIGAN, MARK I. TITLE OF INVENTION: NOVEL FUSE BINDING CTITLE OF INVENTION: PROTEIN AND CDNA THEREFOR NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS: ADDRESSE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK STATE: NEW YORK STATE: NEW YORK COUNTRY: USA ZIP: 10154 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE	Qy 1743 CTCCCACAGGCACCAGCAAACGAATGTAACGTTCCAACACCTGACACAATG 1802	OY 1458 AGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACAGCTGGCCGGTGATTGG 1517 Db 383	

res: 2.06e-14 262.00 arity: 37.56% Austrative: 4.45% D-B (1-3283) x US-08-021-608D-10 (1-643) CCCTCCTCACCTGCAGTGAACACAGAACCCAGAACCAGAAGGTGAACTCACCGGGTTTCCCCTTTCGCTTCCCGGATGAAGAAGCAAAAGAACCACGAAACCAGAACCACAAACCAGAACCACAACCAGAACCACAACCAGAACCACAACCAGAACCACAACA	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDERFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/021,608D FILING DATE: 22-FEB-1993 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: PILING DATE: FILING DATE: CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: WILLIAM S. FEILER REGISTRATION NUMBER: 2026-4063 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 751-6849 INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 643 LENGTH: 643 LENGTH: 643 CTHLED AMID Acid STRANDEDNESS: Single TOPOLOGY: Unknown MOLECULE TYPE: Peptide/Protein MYDOTHETICAL: NO ORIGINAL SOURCE: ORGANISM: Human CELL LINE: HL60 FEATURE: INFORMATION: Amino Acid 148 (Xaa) is Met or Ile OTHER INFORMATION: Amino Acid 148 (Xaa) is Met or Ile
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269SerArgTleGlyGlyAsmGluGlyTleAspNatProfleProArgPheAlava 286 1257 GGGGCCAFTCATCGGGAAGAAGGCGGCACACATCAAACAGCTGGCGAAGATTCGCCGGAGC 1316 286 [GlyTleValIleGlyArgAsmGlyGluMetTleTySLySTIGGIAASnASpAlaGlyVa 306 1317 CTCTATCAAGATTGCCCCTGCGGAAGGCCCAGACGCCAAACGCTGACGAAAGGATGCACCAGACC 1376 1317 CGGGCCACCGGAAGCCCAGTTCAAGGCCCAGACGTCACGAAAGGATGGTCATCATCAC 1376 1317 CGGGCCACCGGAAGCCCAGTTCAAGGCCCAGACGTCACGCGAAAGGATGGTCATCATCAC 1376 1317 CGGGCCACCGGAAGCCCAGTTCAAGGCCCAGA	

Alignment Scores: 2.06e-14 Length: 643 Pred. No.: 262.00 Matches: 140	; OTHER INFORMATION: Amino Acid 148 (Xaa) is Met or Ile US-08-726-160-10	∟ ⊢	원근路	; TYPE: Amino Acid ; STRANDEDNESS: Single ; TOPOLOGY: Unknown	E CHARACTERISTICS: H: 643	; TELEPHONE: (212) 758-4800 ; TELEFAX: (212) 751-8849 ; INFORMATION FOR SEQ ID NO: 10:	14日日	ON: INFO	; APPLICATION NUMBER: 08/021,608 ; FILING DATE: 08/021,608	FILING DATE: 04-OCT-1996 CLASSIFICATION: 435 PRIOR ADDITOTROS	요단	S 23 E	ZIP: 10154 COMPUTER READABLE FORM: MEDIUM TYPE: FICEBUR TICK	NEW YO	ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE	NVENTION: NOVEL FUSE BINDING NVENTION: PROTEIN AND CDNA TH SEQUENCES: 24 FINCE BINESEC	; Patent No. 5734016 ; GENERAL INFORMATION: ; APPLICANT: LEVENS, DAVID L., DUNCAN, ; APPLICANT: ROBERT C., AND AVICAN MARK T	T 1 -72 uen	lyProProAlaProTyrAlaPro	1863 CTGCGGAGGCGAGGACTCTGCCGAGGCCCTGAGAACCCCAGGGGGCCGAGGAGG	,	Qy 1743 CTCCCACAGGCACCAGCAAAACAACGGATGAATGTAGGCCCTTGCAACACGCTGACAGAATG 1802
Db 269SerArgIleGlyGlyAsnĠluGlyIleAspValProllePrOArgPheAlaVa 286 Qy 1257 GGGCGCATCATCGGGAAGAAGGGGGCACACATCAAACAGCTGGCGAGATTCGCCGGAGC 1316 ::: ::: :::::::	257 1197 GCATCAT	1137 TAACACCCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGTTTGGCCCGTTCCC	Qy 1077 TGCTGAGATAGAGATTATGAAGAAGCTGCGTGAGGCCTTTGAAAATGATATGCTGGCTG		GTTGAGGCCTGTGCCAG	Qy 972 ACATGAAACAGGGACCAAGATAACAATCTCATCTTTTGCAGGATTTTGAGCATATACAACCC 1031			QY 862GAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAAAATCTTGGC 911	154	GGGGACTTCTGAAGCATGCCGCATGATTCTTGAAATCATGCAGAAA	QY 756 CCATAGAAAAGAGAACTCTGGAGCTGCAGAGAAGCCTGTCACCATGCCATGCCACCCCAGA 815			Qy 636 CAGACAGATTGATTTCCCGCTGCGGATCCTGGTCCCCACCCA	QY 576 CCAGCGTGGGGACCACTCTTCCCGGGAGCAAGGCCACGCCCCTGGGGGGACTTCTCAGGC 635	Db 59 yTyrGlyGlyGlnLysArgProLeuGluAspGlyAspGlnProAspAlaLysLysValAl 79	3 9	ACCGCCGTTGTCAACGTCACATATGCAAC	Db 10 ProSerSerGlySerAlaGlyGlyGlyGlyGlyGlyGlyGly 22	-09-270-437[Percent Similarity: 37.56% Conservative: 85 Best Local Similarity: 23.37% Mismatches: 237 Query Match: 4.45% Indels: 137 DB: Gaps: 25

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RESULT 14
PCT-US94-01782-10
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APPLICANT:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & D
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                    ZIP:
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                                                                             NEW YORK
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                                                                                                                                                                                                                                                                                                                     Application PC/TUS9401782
                                                                                                                    345 PARK AVENUE
                                                                                                                                                                                                THE GOVERNMENT OF THE UNITED STATES
AS REPRESENTED BY THE SECRETARY, DEPARTMENT
HEALTH AND HUMAN SERVICES
VENTION: NOVEL FUSE BINDING
VENTION: PROTEIN AND CDNA THEREFOR
                                                             USA
                                                                                                                                           MORGAN & FINNEGAN
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Best Local Similarity:
Query Match:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION UNMBER: PCT/US94/01782
FILING DATE: 22-FEB-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 758-48
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO:
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NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
OTHER INFORMATION: Amin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S.
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
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STRANDEDNESS: Sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: WILLIAM S. FEILER REGISTRATION NUMBER: 26, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDIVIDUAL ISOLATE:
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                                                                                                                                                                                                                                                                                                            396 GAATGTGGAACAAGTCAACAGACAGACAGAAACCGCGGTTGTCAACGTCACATATGCAAC 455
                                                                       576 CCAGCGIGGGACCACICTICCCGGGAGCAAGGCCACGCCCCTGGGGGCACTICICAGGC 635
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                                                                                                            59 YTyrGlyGlnLysArgProLeuGluAspGlyAspGlnProAspAlaLysLysValAl
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                                    aProGlnAsnAspSerPheGlyThrGln---
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  TCGTGACCAAACGCCAGATGAAAATGAGGAAGTG---ATCGTCAGAATTATCGGGCAC--
                                         yLysGlyGlyGluThrIleLysSerIleSerGlnGlnSerGlyAlaArgIleGluLeuGl 412
                                                                                     CAAAGGTGGCAAGACCGTGAACGAACTGCAGAACTTAACCAGTGCAGAAGTCATCGTGCC
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                                                                                                                                                                   TELEFAX: (212) 751-6849 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THER.
NUMBER OF SEQUENCES: 24
                TOPOLOGY: Unknow MOLECULE TYPE: Per HYPOTHETICAL: No
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 22-FEB-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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ADDRESSEE: MORGAN & FINNEGAN
                                                                              TYPE: Amino Acid
STRANDEDNESS: Sir
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                               TELEPHONE:
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Best Local Similarity:
Query Match:
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341 GlyGlyArgGlyArgGlyArgGlyGlnGlyAsnTrpAsnMetGlyProProGlyGlyLeu 360
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| AlaValGln-----GluIleMetIleProAlaSerLysAlaGlyLeuValIleGly 186
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                                                        GluIleIleThrAspLeuLeuArgSerValGlnAlaGlyAsnProGlyGlyProGlyPro 340
                                                                                                               ThrThrProGluArgIleAlaGlnileThrGlyProProAspArgCysGlnHisAlaAla 320
                                                                                                                                           GACGTCAGCGAAAGGATGGTCATCATCACCGGGCCACCGGAA----GCCCAGTTCAAGGCC 1404
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                                                                                                                                                                                                                                                                                    -----ArgAsnGluTyrGly-------SerArgIleGlyGlyAsnGluGly 261
                               ---GGACGGATCTTTGGGAAA--
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255.00
38.52%
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Matches:
Conservative:
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Search completed: July 23, 2004, 11:20:10 Job time: 65.5087 secs

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Result
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PODEL=frame+ f2D, model -DEV=xlp

-Q=/cgr2 1/USPTO_spool p/US00270437/runat_23072004_095742_27560/app_query.fasta_1.5582

-DB=Published_Applications_AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1

-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 - MATRIX=blosum62

-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100

-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -UTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0

-MAXLEX=2000000000 -USER-US09270437 @CGN 1 1 35 @runat 23072004 095742 27560

-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100

-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XCAPOP=10 -XGAPEXT=0.5

-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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ALIGNMENTS

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RESULT 1

US-10-97-340-147

Sequence 147, Application US/10097340

Publication No. US20030087250A1

GENERAL INFORMATION:
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Subbangi KAMATKAR

APPLICANT: Steve G. KOVATS
APPLICANT: Hachel E. MEYERS
APPLICANT: Hachel MORRISBY
APPLICANT: Peter OLANDT
APPLICANT: Peter OLANDT
APPLICANT: Gordon B. MILLS
APPLICANT: Gordon B. MILLS
APPLICANT: Robert C. BAST, Jr.
APPLICANT: Rosemarie SCHMANDT
APPLICANT: Karen LU
APPLICANT: Karen CLATT
APPLICANT: Karen GLATT
APPLICANT: Karen GLATT
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR PELLING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/274,967
PRIOR FILING DATE: 2001-03-14
PRIOR PELLING DATE: 2001/09/26
PRIOR PELLING DATE: 2001/09/26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR APPLICATION NUMBER: 60/323,102
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 147
LENGTH: 556
                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo
US-10-097-340-147
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Best Local Similarity:
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Pred. No.:
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US-10-648-593-182
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US-10-648-593-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION: INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS: TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OI TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS CURRENT APPLICATION NUMBER: US/10/648,593

CURRENT APPLICATION NUMBER: 60/406,385

PRIOR APPLICATION NUMBER: 60/406,385

PRIOR FILING DATE: 2002-08-27

NUMBER OF SEQ ID NOS: 557

SOFTWARE: Patentin version 3.2

LENGTH: 556

TUTDE: NDT
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ORGANISM: Homo
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                        {\tt HisAlaProGlyGlyThrSerGlnAlaArgGlnIleAspPheProLeuArgIleLeuVal}
                                                                                                                                                                                              GCCGTTGTCAACGTCACATATGCAACAAGAGAAGAAGCAAAAATAGCCATGGAGGAAGCTA
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APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1116
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CURRENT APPLICATION NUMBER: US/10/262,445
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 60/327,454
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,449
PRIOR APPLICATION NUMBER: 60/329,414
PRIOR APPLICATION NUMBER: 60/329,414
PRIOR APPLICATION NUMBER: 60/339,142
PRIOR PILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 60/330,142
PRIOR APPLICATION NUMBER: 60/330,142
PRIOR APPLICATION NUMBER: 60/330,142
PRIOR APPLICATION NUMBER: 60/341,058
PRIOR APPLICATION NUMBER: 60/341,058
PRIOR APPLICATION NUMBER: 60/344,059
PRIOR APPLICATION NUMBER: 60/349,575
PRIOR PILING DATE: 2001-10-24
PRIOR PILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 60/349,575
PRIOR PILING DATE: 2001-10-29
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APPLICANT: Blrgess, Catherin
APPLICANT: Catterton, Elina
APPLICANT:
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APPLICANT:
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 133
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 40
LENGTH: 555
TYPE: PRT
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APPLICANT: Zhong, Mei
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND
TITLE OF INVENTION: THE SAME
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                                                                   PRIOR APPLICATION NUMBER: 60/349,575 PRIOR FILING DATE: 2001-10-29
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Gerlach, Valerie
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Taupier Jr., Raymond
Zerhusen, Bryan
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Patturajan, Meera
Rieger, Daniel
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Mezes, Peter
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Best Local Similarity:
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                                                                  CCTGTCACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATGATTCTTGAA
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GENERAL INFORMATION:

APPLICANT: MCNAb, Andria

APPLICANT: MCNAb, Andria

APPLICANT: McNab, Andria

APPLICANT: Metanabe, Yoshihiro

APPLICANT: Reed, Steven G.

APPLICANT: Wang, Tongtong

ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C19

CURRENT APPLICATION UNMBER: US/10/313,986

CURRENT FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 560

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 500

LENGTH: 577

TYPE: PRT
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US-10-313-986-500
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; SEQ ID NO 2; LENGTH: 577; TYPE: PRT; ORGANISM: Mus musculus US-09-873-637-2
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                                                                                                                            Sequence 2, Application US/09873637
Patent No. US20020061543A1
GENERAL INFORMATION:
                                              APPLICANT: ROSS, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
FILE REFERENCE: 960296.95131
CURRENT PAPPLICATION NUMBER: US/09/873,637
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: MCNAbb, Andria
APPLICANT: WcNabb, Andria
APPLICANT: Watamabe, Yoshihiro
APPLICANT: Watamabe, Yoshihiro
APPLICANT: Watamabe, Yoshihiro
APPLICANT: Wang, Tongtong
ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
ITITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C19
CURRENT APPLICATION NUMBER: US/10/313,986
CURRENT FILLY DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOPTWARE: FASTSEQ for Windows Version 4.0
IENGTH- 589
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Best Local Similarity:
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RESULT 9
US-09-735-705-348
                                                                           Sequence 348, Application US/09735705 Patent No. US20020052329A1
                                               APPLICANT:
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Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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                                   Kalos, Michael D.
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Panger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
FURBENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
ROPHMENDE: Pascero for Windows Version 2 0
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Skeiky, Yas
                                                                   ArgGlnGly---SerProGlySerValSerLysGlnLysProCysAspLeuProLeuArg
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CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
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                                                                     ArgGinGly---SerProGlySerValSerLysGlnLysProCysAspLeuProLeuArg
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APPLICANT: Vedvick, Thomas S.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Henderson, Robert A.

APPLICANT: Henderson, Robert A.

APPLICANT: Peckham, David W.

APPLICANT: Peckham, David W.

APPLICANT: Peckham, David W.

APPLICANT: Penger, Neil

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCE FILE REFERENCE: 210121.455C16

CURRENT APPLICATION NUMBER: US/9/897,778

CURRENT FILING DATE: 2001-06-28

NUMBER OF SEQ ID NOS: 467

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 348

LENGTH: 579

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                               GlnGlnAsnProLeuGlnGlnProArgGlyArgArgGlyLeuGlyGlnArgGlySerSer
                                                                    TCCCCTTCGCCCCTCAG-----CGAGCCCAGCGT------GGGGACCACTCTTCCCGG
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 ATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCAGGGAAATTGTACAA
                                               GCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTCAGA
                                                                                                            TTCTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACA
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APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Panger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 446
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
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: Watanabe, Yoshihiro
GGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGATGAAGAGGTGAGC
                                            ValValAsnValThrTyrSerSerLysAspGlnAlaArgGlnAlaLeuAspLysLeuAsn
                                                                GTTGTCAACGTCACATATGCCAACAAGAGAAGAAGCAAAAAATAGCCATGGAGAAAGCTAAGC
                                                                                                         CTCTTTGGGGACAGGAAGCTGCCCCTGGCGGGACAGGTCCTGCTGAAGTCCCGGCTACGCC
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TTCTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACA
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APPLICANT: Wang, Tongtong
APPLICANT: Warnerakis, Margarita
APPLICANT: Marnerakis, Margarita
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILTE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 449
LENGTH: 579
TYPE: PRT
ORGANISM: Homo canican
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CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 348
LEUGTH: 579
TYPE: PRT
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APPLICANT: Foy, Teresa M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121,455C17
FILE REFERENCE: 120121,455C17
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Retter, Marc W.
Durham, Margarita
Fanger, Gary R.
Vedvick, Thomas S.
Carter, Darrick
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C17
CURRENT PLICATION NUMBER: US/10/007,700
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 446
ENGTH: 579
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Listing first 45 summaries
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-MODEL=frame+_n2p.model -DEV=xlp
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ALIGNMENTS

hypothetical protein M88.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T23837
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R; 밁 Ś 밁 Ş RESULT 1 T23837 US-09-270-437D-8 (1-3283) x T23837 (1-854) Percent Similarity:
Best Local Similarity:
Query Match: A;Map position: 3 A;Introns: 38/3; 96/1; 133/3; 255/3; A; Molecule type: DNA A; Residues: 1-854 <WIL> Score Alignment Scores: A; Gene: CESP: M88.5 A; Experimental source: clone A; Cross-references: EMBL: Z34802; A;Status: preliminary; translated from GB/EMBL/DDBJ A;Reference number: Z19806 A;Accession: T23837 ;Genetics: No.: 264 GlnGlnHisGlnAlaGlyGlnHisGlnGlnSerHisHisGlnSerGlnAsnHisAsn---460 GAAGAAGCAAAAATAGCCATGGAGAAGCTAAGCGGGCATCAGTTTGAGAACTACTCCTTC 519 422 CAGAAACCGCCGTTGTCAACGTCACATATGCAACAAGA---GinHisProGlnMetMetGlnGlnHisAlaGlnGlnGlyTyrHisProHisGlnGlnAsn 1.48e-24 474.50 40.17% 25.71% 8.06% M88 PIDN: CAA84338.1; GSPDB: GN00021; CESP: M88.5 307/3; 395/2; Gaps: Length: Matches: Mismatches: Indels: Conservative: 436/2; 492/3; 657/3; 759/1; 820/1 854 153 86 176 181 263 459

1350	CAAGATTGCCCCTGCGGAAGGCCCAGAC 1 11ysIleGluAlaProGluGluLysThrGlnArgG	11G	1234	Ľ · Þ	hrProValGlyValMetGl	6ATGCTGGCTGTTAACACCCACTCCGG	GCTGCGTGAGGCCTTTGAAA :::::: sLeuLysLysCysTyrGlus	1042 ATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCTGAGATAGAGATTATGAAG 	1027 AACCCG	AACAGG : sThrGl	907 TTGGCACACTGGCTTGGTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTGAAGAAA 	853 ATGCAGAAAGAGGCAGATGAGACCAAACTAGCCG ::: 384 IleGInSerGluAlaValLysAspAspValAsnValGlyA	793 GTCACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATGATTCTTGAAAT ::: :::	748 GTAGATATCCATAGAAAAGAGAACTCTGGAGCTGCAGAGAAGCCCG	688 GCCATCATCGGAAAGGAGGGCTTGACCATAAAGAACATCACTAAGCAGACCCAGTCC	634 GCCAGACAGATTGATTTCCCGCTGCGGATCCTGGTCCCCACCCAGTTTGTTGGT	580 CGTGGGGACCACTCTTCCCGGGAGCAAGGCCACG(283
1350	13 luAlaGluGluAlaGluLysLys 61	rGLy	TTCATCCCAACCCAGGCTGTGGGC 1260 ::::: :::pValProAspSerMetIleGly 579		 	racc Vals	laGlnSerMetGlnCysPro 499	CTGAGATAGAGATTATGAI aGluAlaLeuIleSerAl	GAAAGAACC 1041 euLeuGlyLeuMetGluArgThr 459	CTTTGCAGGATTTGAGCATATAC 1026	AAGAAGGCAGAAATTTGAAGAAA 966 ::::: ::: ,ysAlaGlySerSerIleLysGlu 423	GATGAGACCAAACTAGCCGAAGAGATTCCTCTGAAAATC 906 ::: :::: ::::: AspAspValAsnValGlyAlaAspThrValLeuArgMet 403	CATGCCGCATGATTCTTGAAATC 852 	GAGCTGCAGAGAAGCCT 792 alLeuGlyAsnAsnAspArgIle 363	TCACTAAGCAGACCCAGTCCCGG 747	TGGTCCCCACCCAGTTTGTTGGT 687 :: alValGluGlyLysTyrHisAla 323	AAGGCCACGCCCCTGGGGGCACTTCTCAG 633	-Gln 2

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US-09- Qy Db	est con	RESULT T19216 hypothe C;Speci C;Date: C;Acces R;McMur submitt A;Refer A;Reseid A;Statu A;Molec A;Cross A;Exper C;Genet A;Gene: A;Map p A;Intro	Db Qy	g dg	Qу	Qy Db	Qγ	Qy Db	D A A	g Q	Db &	Ov Db
9	it Scores: 8.49e-11 L 5.: 274.00 M Similarity: 41.13% C cal Similarity: 24.63% M atch: 4.66% G	RESULT 2 T19216 T19216 Appothetical protein C12D8.1a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T19216 R;McMurray, A: submitted to the EMBL Data Library, June 1996 A;Reference number: Z19092 A;Accession: T19216 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Mclecsion: T19216 A;Residues: 1-589 <wild- 159="" 1;="" 25="" 2<="" 318="" 3;="" 5="" 513="" 7="" a;cross-references:="" a;experimental="" a;genet="" a;introns:="" a;map="" c12d8="" c;genetics:="" cesp:c12d8.1a="" clone="" embl:z73969;="" gspdb:gn00023;="" pidn:caa98232.1;="" position:="" source:="" td=""><td>1696 GAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCGAGCAAGT 1738 </td><td>1654 CAGCGCAAGATCAGGGAAATTGTACAACAGGTGAAGCAGCAG 1695</td><td>1597GAAAATGAGGAAGTGATCGTCAGAATTATCGGGGCACTTCTTTGCTAGCCAGACTGCA 1653 </td><td>1564 GAAGTCATCGTGCCTCGTGACCAAACGCCAGAT</td><td>1504 GGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGAAC</td><td>1453AAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACAGCT 1503</td><td>1408 GGACGGATCTTTGGGAAACTGAAAGAGGAAAACTTCTTTAACCCC</td><td>1351GTCAGCGAAAGGATGGTCATCATCACCGGGCCACCGGAAGCCCAGTTCAAGGCCCAG 1407 </td><td>640 GluPheLeuGluAspAsnAlaThrIleAsnSerSerAspAlaIleGluGluLysProLys</td><td>620 ArgLysLeuAspGluThrAspSerGlyCysGluGlyValAlaSerGlyAspHisProGln 639</td></wild->	1696 GAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCGAGCAAGT 1738	1654 CAGCGCAAGATCAGGGAAATTGTACAACAGGTGAAGCAGCAG 1695	1597GAAAATGAGGAAGTGATCGTCAGAATTATCGGGGCACTTCTTTGCTAGCCAGACTGCA 1653	1564 GAAGTCATCGTGCCTCGTGACCAAACGCCAGAT	1504 GGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGAAC	1453AAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACAGCT 1503	1408 GGACGGATCTTTGGGAAACTGAAAGAGGAAAACTTCTTTAACCCC	1351GTCAGCGAAAGGATGGTCATCATCACCGGGCCACCGGAAGCCCAGTTCAAGGCCCAG 1407 	640 GluPheLeuGluAspAsnAlaThrIleAsnSerSerAspAlaIleGluGluLysProLys	620 ArgLysLeuAspGluThrAspSerGlyCysGluGlyValAlaSerGlyAspHisProGln 639

	1234 CTCTTCATCCCAACCCAGGCTGTGGGGGCCATCATCGGGAAGAAGGGGGCACATCAAA 1293 :::	997 ATCTCATCTTTGCAGGATTTGAGCATATACAACCCGGAAAGAACCATCACCTGTGAAG 1053 ::: ::: 168 LeuValGlnAspAsnGlnSerValSerAspGlnSerLysProLeuArgIleThr 185 1054 GGCACAGTTGAGGCCTGTGCCAGTGCTGAGATTATGAAGAACCTGCGTGAGGCC 1113	727 ACTAAGCCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAAACTCTGGAGCTGCAGAG 786 :::
Qy 727 ACTANGCAGACCCAGTCCCGGGTAGATACAAGAGAACTCTGGAAGCTGCAGAGTCATGAAAAAAAA	A; Gene: CESP:C12D8.1b A; Map position: 5 A; Introns: 181/3; 340/3; 535/2 Alignment Scores: 8.58e-11 Length: 611 Score: 274.00 Matches: 118 Perd. No.: 274.03 Matches: 79 Perst Local Similarity: 24.63\$ Mismatches: 183 Query Match: 4.66\$ Indels: 99 DB: 2 Gaps: 18 US-09-270-437D-8 (1-3283) x T19217 (1-611) Qy 667 GTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAAGG	RESULT 3 T19217 T19217 hypothetical protein C12D8.1b - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: T19217 R;McMurray, A. submitted to the EMBL Data Library, June 1996 A;Reference number: Z19092 A;Accession: T19217 A;Accession: T19217 A;Accession: T19217 A;Accession: T19217 A;Gession: DA A;Residues: 1-611 <wil> A;Cross-references: EMBL: Z73969; PIDN:CAA98233.1; GSPDB:GN00023; CESP:C12D8.1b A;Experimental source: clone C12D8 C;Genetics:</wil>	Db 394

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                                                                                                               CGAGGCCCTGAGAACCCCAGGGGGCCCAAGGAGGGCGGGGAAGGTCAGCCAGGTTTGCCAG
                                                                                                                                                                                        GGAGCAAACCAAAGACCATCTGAGGAATGAGAAGTCTGCGGAGGCGGCCAGGGACTCTGC
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hypothetical protein F8M21.160 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Uun-2000 #sequence_revision 02-Uun-2000 #text_change 02-Uun-2000 C;Accession: T49962 R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; submitted to the Protein Sequence Database, April 2000 A;Reference number: Z24493 A,Accession: T49962 A,Status: preliminary
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A;Residues: 1-568 <BEV>
A;Cross-references: EMBL:AL353993; GSPDB:GN00063; ATSP:F8M21.160
A;Experimental source: cultivar Columbia; BAC clone F8M21
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Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: D96554
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A;Molecule type: DNA
A;Residues: 1-621 <STO>
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R;Duncan, R.; Bazar, L.; Michelotti, G.; Tomonaga, T.; Krutzsch, H.; Avigan, M.; Levens, Genes Dev. 8, 465-480, 1994
A;Title: A sequence-specific, single-strand binding protein activates the far upstream e. A;Reference number: A53184; MUID:94170991; PMID:8125259
A;Accession: A53184
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A53184
Myc far upstream element-binding protein - human
MyAlternate names: FUSE-binding protein
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
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C;Date: 06-Jan-1995 #text_change 05-Nov-1999
C;Date: 06-Jan-1995 #text_change 05
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Best Local Similarity:
Query Match:
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A;Residues: 1-644 <DUN>
A;Cross-references: GB:U05040; NID:g460151; PIDN:AAA17976.1;
C;Keywords: DNA binding
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hypothetical protein ZK418.9 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t-
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A; Residues: 1-768 < FUL>
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                                                                                                                              ACAACCCGGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGT-
                                                  CCAGTGCTGAGATAGAGATTATGAAGAAGCTGCGTGAGGCCTTTGAAAATGATATGCTGG 1132
                                                                                      al-----GlnGluThrThrThrAlaThrGlyGlnProLysProLeuArgMetIleGlyS 404
                                                                                                                                                                            leValGlnGluGlnSerGly---
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hypothetical protein M01A10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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A;Molecule type: DNA
A;Residues: 1-680 <SCH>
A;Cross-references: EMBL:U88174; PIDN:AAB42272.1; GSPDB:GN00019; CESP:M01A10.1
A;Experimental source: strain Bristol N2; clone M01A10
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| CysGlyAlaIleIleGlyLysLysGlyGluGlnMetArgLysLeuArgSerTrpThrAsn 273
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A;Residues: 1-398 <LYN>
A;Cross-references: EMBL:AL031825; PIDN:CAA21234.1; GSPDB:GN00068; SPDB:SPCC757.09c
A;Experimental source: strain 972h-; cosmid c757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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LeuAlaSerThrAlaSerProGlnGlnValSerProProAlaAlaProSerThrThrSer
                                                                                                                                                                                                                TCATCTTTGCAGGATTTGAGCATATACAACCCGGAAAGAACCATCACTGTGAAGGGCACA
                                                                                {\tt ArgGlyAlaGlyThrValPheTyrAsnProValSerArgLeuThrGlnProLeuProSer}
                                                                                                                                                                                                                                                              Ser-----LysAspMetLeuProGlnSerThrGluArgThrValGluIleHisGlyThr
                                                                                                                                                                                                                                                                                                                                                   GlyArgAsnGlyLeuArgIleLysLeuIleGlnAspLysCysSerCysArgMetIleAla
                                                                                                                                                                                                                                                                                                                                                                                                 GGAAAAGAAGGCAGAAATTTGAAGAAAATTGAACATGAAACAGGGACCAAGATAACAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCATGATTCTTGAAATCATGCAGAAAGAGGCA-----
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                                                                                                                                                                       ValAspAsnLeuHisAlaAlaIleTrpGluIleGlyLysCysLeuIleAspAspTrpGlu
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probable RNA-binding protein - Arabidopsis thaliana N;Alternate names: protein T32M21.30 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 # (PAccession: T48439 R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C. ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X. submitted to the Protein Sequence Database, March 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 Superior Research 20 
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A; Note: T32M21.30
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A;Experimental source: cultivar Columbia; BAC clone T32M21
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A; Residues: 1-313 <BEV>
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---TCTGGAGCTGCAGAGAAGCCTGTCACCATCCATGCCACCCCAGAGGGGGACTTCTGAA 828
                                                    {\tt IleThrGluPheGlnAlaLysSerGlyAlaArgIleGlnLeuSerArgAsnGlnGluPhe}
                                                                                                                  ATAAAGAACATCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAAC---
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C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: C86275
C;Accession: C86275
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Chin, C.W.; Chung, M.K.; Comn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
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Rizzo, M.; Roomey, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Roomey, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Roomey, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Roumey, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Roume, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Roume, T.; Rowley, D.; Sakano, H.
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A; Residues: 1-479 <STO>
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193 LeuSerHisAspGluheuLeuHeuIleIleGlyGluProLeuValValArgGluÄlaLeu 1117 GAAAATGATATGCTGGCTGTTÄACACCCACTCCGGATÄCTTC	22.20% 3.98% 3.98% 2 28275 (1-4 CTCTTCCCGGGAGCAAG ::: :::::::::::::::::::::::::::::	. No.: 4.19e-08 Length: 2: 234.50 Matches: 2nt Similarity: 42.38% Conservative:
Pred. No.: 8.87e-08 Bescre: 229.50 Matches: 105 Percent Similarity: 42.208 Best Local Similarity: 24.088 Mismatches: 179 Percent Similarity: 24.088 Mismatches: 179 Percent Similarity: 24.088 Mismatches: 179 Percent Similarity: 108 Percent Similarity: 108 Percent Similarity: 109 24.088 Mismatches: 179 Percent Similarity: 109 523 ATTTCCTACATCCCGGATGAAGAGGTGAGCCCCCTCAGCGAGCCCAGCGT 10	1390 331 Va 331 Va 11441 TT 351 355 I1 1561 GC 365 II 16612 AF	Qy 1354 AGCGAAAGGATGGTCATCATCACCGGGGCCACCGGAA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ileSerArgIleLysSerGluThrSerAlaArgIleAsnIleSerAsnAsnIleArg---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACCCCCATCACCAGTTTGGCCCGTTCCCGCAT-----CATCACTCTTATCCAGAG 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTGCCAGTGCTGAGATAGAGATTATGAAGAAGCTGCGTGAGGCCTTTGAAAATGATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gln-----LeuLeuLeuSerAsnAspArgIleLeuThrIleAsnGlyValProAspAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGGATTTGAGCATATACAACCCGGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlySerArgLeuArgGluIleGluAspLeuSerAlaAlaLysLeuPheAlaSerProAsn 187
                                                                                      LeuThrileArgGlyThrPheMetAlaSerGlnAlaAlaIleMetLeuIleSerAsnLys
                                                                                                                                                                             GlyCysSerIleIleIle-----GinAspProValGluGlySerSerGluArgArg 377
                                                                                                                                                                                                                       AGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAA---AATGAGGAAGTGATC 1614
                                                                                                                                                                                                                                                                                                              AACTTCTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCC 1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGCCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAAGAGGAA 1437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCAAGATTGCCCCTGCGGAAGGCCCCAGAC---GTCAGCGAAAGGATGGTCATCATCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IleAspHisSerGlnProAsnThrIlePheHisGlnArgAsnHisGlnTyrHisProSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IleHisIleAlaThrPheTyrIleSerGlnThrLeuLeuAsn---PheGlnMetGluSer 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCAGAAATTTGAAGAAAATTGAACATGAAACAGGGACCAAGATAACAATCTCATCTTTG 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PheValGlyAsnValIleGlyLysAspGlyLysHisIleAsnSerValLysGluSerThr
                                                                                                                                                                                                                                                                                                                                                               IlePheIleAspGluLys----
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyProValIleSerProAlaProGlyAsnHisLeuLeuMetAsnPheValGlnGlnGlu 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCGGGAAGAAGGGGGCACACATCAAACAGCTGGCG-----AGATTCGCCGGAGCCTCT 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspLysLeuLeuSerTyrLysProAsnLysAsnLeuProIleSerSerThr-----
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  Ile--
                                          ATCAGGGAAATTGTACAACAGGTGAAGCAGCAGGAGCAGAAATACCCT
                                                                                                                              GTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCA---
-GluIleAspArgSerAsnAlaGluArgLysArgArgSerPro
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C;Species: Homo sapiens (man)
C;Date: 15-Feb-1996 #sequence revision 01-Mar-1996 #text_change 01-Dec-2000
C;Date: 15-Feb-1996 #sequence revision 01-Mar-1996 #text_change 01-Dec-2000
C;Accession: S58529; S58523; S56678; S43489; S41378; S42472
R;Kiledjian, M.; Wang, X.; Liebhaber, S.A.
RMBO J. 14, 4357-4364, 1995
A;Title: Identification of two KH domain proteins in the alpha-globin mRNP stability comparation in the stability comparation of two KH domain proteins in the sipha-globin mRNP stability comparations in the sipha-globin mRNP stability comparations (S58523; MUID:96016208; PMID:7556077
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A;Molecule type: protein
A;Residues: 125-139,251-265;315-323 <KI2>
A;Residues: 125-139,251-265;315-323 <KI2>
B;Leffers, H.; Dejgaard, K.; Celis, J.E.
Eur. J. Biochem. 230, 447-453, 1995
Eur. J. Biochem. 230, 447-453, 1995
A;Title: Characterisation of two major cellular poly(rC)-binding human proteins, each co
A;Title: Characterisation of two major cellular poly(rC)-binding human proteins, each co
A;Reference number: 865678; MUID:95331278; PMID:7607214
A;Accession: 865678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Aasheim, H.C.; Loukianova, T.; Deggerdal, A.; Smeland, E.B.
Nucleic Acids Res. 22, 959-964, 1994
A;Title: Tissue specific expression and cDNA structure of a human transcript encoding A;Reference number: $43489; MUID:94203810; PMID:8152927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X78137; NID:g460770; PIDN:CAA55016.1; PID:g460771
A;Experimental source: AMA cells (transformed human amnion cells)
A;Note: submitted to the EMBL Data Library, March 1994
A;Note: submitted to the
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A; Residues: 1-356 < KIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-298, 'H' <AAS>
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A; Residues: 1-204,'V',206-356 <LEF>
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C;Keywords: RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: GDB: HNRNPX
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DB:
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Best Local Similarity:
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GlyAlaArgIleAsnIle-
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AAAGAGGCAGATGAGACCAAACTA-
                                                       LeuThrGlyProThrAsnAlaIlePheLysAlaPheAlaMetIleIleAspLysLeuGlu 80
                                                                                                                     ATCCATGCCACCCCAGAGGGACTTCTGAAGCATGCCGCATGATTCTTGAAATCATGCAG 858
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      -GCCGAAGAGATTCCTCTG 900
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A;Reference number: Z13377

A;Accession: T04533

A;Molecule type: DNA
A;Residues: 1-846 <BEV>
A;Cross-references: EMBL:AL021710

A;Experimental source: cultivar Columbia; BA
C;Genetics:
A;Map position: 4
A;Introns: 94/3; 140/3; 161/3; 191/3; 232/3;
A;Note: F28J12.30
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                                                                                                                                                                                                                                                                                                                        TTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAAGAGGAA
                                                                                                                                                                                                                                                                                                                                                       ValGluGlySer-
                                                                                                                                                                                                                                                                                                                                                                              GCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCACCGGGCCACCGGAAGCCCAG 1395
                                                                                                                                                                                                                                                                                                                                                                                                         GlyAlaAsnIleAsnGluIleArgGlnMetSerGlyAlaGlnIleLysIleAlaAsnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGGCACACATCAAACAGCTGGCGAGATTCGCCGGAGCCTCTATCAAGATTGCC---CCT 1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlnThrThrHisGluLeuThrIleProAsnAsnLeuIleGlyCysIleIleGlyArgGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGAGATIGIGAAICTCITCATCCCAACCCAGGCIGIGGGCGCCATCATCGGGAAGAAG 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyIleAspSerSerProGluValLysGlyTyrTrpAlaSerLeuAspAlaSerThr
                                                                                                                                                                                                                                                                                           SerLeuAlaGlnTyrLeuIleAsnAlaArgLeuSerSerGlu
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                              _140/3; 161/3; 191/3; 232/3; 262/1; 287/1; 293/3; 300/3; 503/3;
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                                                      AspAsnValValIleSerGlyGluProGluSerValLysGlnAlaLeuPheAlaVal
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RESULT 15
A44125
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A44125
C;Accession: A44125
R;McKnight, G.L.; Reasoner, J.; Gilbert, T.; Sundquist, K.O.; Hokland, B.; McKey, M. Biol. Chem. 267, 12131-12141, 1992
A;Title: Cloning and expression of a cellular high density lipoprotein-binding A;Accession: A44125; MUID:92291094; PMID:1318310
A;Accession: A44125
A;Status: preliminary
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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A;Residues: 1-1268 <MCK>
A;Residues: 1-1268 <MCK>
A;Cross-references: GB:M64098; GB:M83789; NID:g183891; PIDN:AAA35962.1; PI
A;Note: sequence extracted from NCBI backbone (NCBIN:106862, NCBIP:106863)
C;Superfamily: vigilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-270-437D-8 (1-3283) x A44125
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                                                                                                                                AlaGluAsnSerAsnSerGluThrIleIleIleThrGlyLysArgAlaAsnCysGluAla
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CTGGCTGTTAACACCCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGTTTGGC 1188
                                       AlaArgSerArgIleLeuSerIleGlnLysAspLeuAlaAsnIleAlaGlu------
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1249 CAGGCTGTGGGCGCATCATCGGGAAGAAGAGGGGGCACACATCAACAGCTGGCAAGATTCATCGGGAAGAAGAGGGGGCACACATCAACAGCTGGCGAAGATTC 1308 ::::::::::::::::::::::::::::::::::::
CAGGCTGTGGGGCCATCATCGGGAAGAAGGGGGCACACATCAAACAGCTGGCGAGATCATCGAAGAAGGGGGCACACATCAAACAGCTGGCGAAGATCATCGAAACAGCTGGCGAAGATCATCAAACAGCTGGCGAAGATCCCCTGCGGAAGAACAGCTCAAACAGCTGGCGAAGGATCC ::::::
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Search completed: July 23, 2004, 11:18:18 Job time: 80.5997 secs

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Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09270437/runat_23072004_095739_27413/app_query.fasta_1.5582
-DB-SwissProt_42_-ORMT=fastan -SUFFIX=rsp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pot -THR_MAX=100 -THR_MIN=0 -ALICN=15 -MODE=LOCAL
-UCTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=2000000000
-USER=US09270437_@CGN_1_1_57 @runat_23072004_095739_27413 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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No.
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , I
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5.6.7.7.8.8.9.9.0.1
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Copyright (c) 1993 - 2004 Compugen Ltd.
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FUB2 RAT
FUB1 HUMAN
FUB1 MOUSE
FUB2 HUMAN
ZBP2 CHICK
Y475 ARATH
PCB3 HUMAN
PCB4 HUMAN
PCB4 HUMAN
PCB1 RABTT
VGLN HUMAN
PCB1 RABTT
VGLN HUMAN
PCB4 HUMAN
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PCB4 HUMAN
PCB1 RABTT
VGLN HUMAN
PCB4 HUMAN
PCB4 HUMAN
PCB4 HUMAN
PCB4 HUMAN
PCB4 HUMAN
PCB5 RABTT
VGLN HUMAN
PCB4 MOUSE
NOA2 HUMAN
PCB2 MOUSE
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Q99pf5 rattus norv
Q96ae4 homo sapien
Q91wj8 mus musculu
Q92945 homo sapien
                                                         Q00341
Q80wa4
P57724
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O19048
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P58223
P57722
P57721
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P38151
                               Q9unw9
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rattus norv
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gallus gall
arabidopsis
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homo sapien
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147	148	148.5	148.5	149.5	149.5	150.5	152	152.5	153.5	156	157	160.5	160.5	166	167	170.5	172	173	173	180	184	187.5	207	207	207.5	210
2.5	2.5	2.5	2.5	2.5	2.5	2.6	2.6	2.6	2.6	2.7	2.7	2.7					2.9					3.2				3.6
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YAV2_XANCV	MRTB_MOUSE	Y8B7_BACTN	ELV3 HUMAN	MINT HUMAN	ATX7 MOUSE	YO62 DEIRA	ATX7 HUMAN	PABP SCHPO	MLL2 HUMAN	PC15 MOUSE	VIT2_CHICK	AK12_HUMAN	NR54 HUMAN	APC_RAT	PCLO_HUMAN	YBD2_YEAST	YHLI_EBV	ROK RABIT	ROK HUMAN	S160_YEAST	PAB2 ARATH	TDRH HUMAN	VGLN CHICK	NOA1 HUMAN	NOA1 MOUSE	PCB2_HUMAN
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ALIGNMENTS

RT	RA	RA RA	RA S	PA A	RA	RA	2 3	RA	RA.	R A	RA	RA	RX	RC C	RP	d i	<u> </u>	RT	RA	RX	ŖР	RN	2 6	88	SO	Ω¦	J F	1 5	Ţ	ΑĊ	RESULT FUB3_H	
"Generation and initial analysis of more than 15,000 full-length	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,		Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	.A.,	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	Raha S.S., Loquellano N.A., Peters G.J. Abramson R n. Mullahy G.,	asavant T.L., Scheet	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	Honking R F. Jordan H. Moore T. Mark T. Warr T. Traigh R. K.,	F.S., Wagner L., Shenmen C.M., S	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	MEDLINE=22388257; PubMed=12477932;	Placenta:	SEOUENCE FROM N.A. (ISOFORMS 1 AND 2)	[2] DIVI. CHEM. 4/1:310/9-3100/(1990).		rise an ancie	Davis-Smyth T., Duncan R.C., Zheng T., Michelotti G., Levens D.:	MEDLINE=97094955; PubMed=8940189;	SEQUENCE FROM N.A. (ISOFORM 1).		NCBI Tavillació.	Chordata;	Homo sapiens (Human).	FUBP3.	himbing market	10-OCT-2003 (Rel. 42, Last sequence update)	10-OCT-2003 (Rel. 42, Created)	FORS_HUMEN SIANUARU; PRI; 572 AA.	LT 1 HUMAN	

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Percent Similarity:
Best Local Similarit
Query Match:
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-!- FUNCTION: May interact with single-stranded DNA from tupstream element (FUSE). May activate gene expression.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50084; KH TYPE 1; 4.
Transcription regulation; Trans-acting factor; Nuclear protein; DNA-binding; Repeat; Alternative splicing.
DOMAIN 77 141 KH 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00013; KH; SMART; SM00322; KH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U69127; AAC50893.1; ALT_FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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InterPro; IPR004088; KH_type_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q96124-2; Sequence=VSP_008323, VSP_008324;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Detected in a number of cell lines.
SIMILARITY: Contains 4 KH domains.
CAUTION: Ref.1 sequence differs from that shown due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 frameshift in position 18.
CAUTION: Ref. 2 (AAH01325) sequence differs from that shown a frameshift in position 527.
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                             CATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGATGAAGAGGTGAGCTCC
                                                         SerThr-ProLeuValAspProSerValTyrGlyTyrGlyValGlnLysArgProLeuAs
                                                                                     CCTTCGCCCCCTCAGCGAGCCCAGCGTG---
pAspGlyValGlyAsnGlnLeuGlyAlaLeuValHisGlnArgThrValIleThrGlu--
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214 IleThrGlyAspAlaPheLysValGlnGlnAlaArgGluMetValLeuGluIleIleArg
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                                                                                                                                                                                                                                                                                                                                   GCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCACCGGGCCACCGGAAGCCCAG 1395
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                                                 GTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTCAGAATTATCGGGCAC 1632
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PROSITE; PS50084; KH TYPE 1; 4
Transport; mRNA transport; mRNI
Transcription regulation; Trans
DNA-binding; RNA-binding; Repe-
DOMAIN 145 209 K
DOMAIN 234 300 K
DOMAIN 323 387 K
                                                                                                  Pfam; PF00013; KH; SMART; SM00322; KH;
                                                                                                                                                                                                                                                                                                                                                                                    J. Neurochem. 82:1039-1046(2002).

-!- FUNCTION: Part of a ternary complex that binds to the downstre control sequence (DCS) of the pre-mRNA. Mediates exon inclusic transcripts that are subject to tissue-specific alternative splicing. May interact with single-stranded DNA from the farupstream element (FUSE). May activate gene expression (By similarity). Binds to the dendritic targeting element and may
                                                                                                                                  InterPro; IPR004088;
                                                                                                                                            EMBL; AF308818; AAG59811.1; -. InterPro; IPR004087; KH_dom.
                                                                                                                                                                                      entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                 use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                   a role in mRNA trafficking.

-!- SUBUNIT: Part of a ternary complex containing FUBP2, and HNRPH1 (By similarity).

-!- SUBCELLULAR LOCATION: Nuclear. A small proportion is the cytoplasm of neuronal cell bodies and dendrites.

-!- SIMILARITY: Contains 4 KH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rehbein M., Wege K., Buck F., Schweizer M., Richt "Molecular characterization of MARTA1, a protein dendritic targeting element of MAP2 mRNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Far upstream element binding protein 2 (FUSE binding protein 2)
type splicing regulatory protein) (KSRP) (MAP2 RNA trans-acting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22246918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUBP2 OR KHSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein 1) (MARTA1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q99PF5;
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUB2_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=12358751;
                                                                                                                                                                                                                                institutions as long
                                                                                                                            KH_type_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----ArgArgPheThrIleArgGlyValProGlnGlnIleGluVal
 ; Trans-acting; Repeat. KH 1. KH 2. KH 3.
                                                                      mRNA processing; mRNA
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Sciurognathi; Muridae
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                                                        factor;
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        euThrGlyAlaProGluSerValGlnLysAlaLysMetMetLeuAspAspIleValSerA
                                  TCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATGATTCTTGAAATCATGCAGA
                                                                                                                   etValGlyLeuTleTleGlyArgGlyGlyGluGlnIleAsnLysIleGlnGlnAspSerG
                                                                                                                                                 TTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGAACATCACTAAGCAGACCC
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                                                                                        AGTCCCCGGTAGATATCCATAGAAAAGAGAACTCTGGAGCTGCAGAGAAGCCCTGTCACCA
                                                                                                                                                                                roArgThrSerMetThrGluGlu-
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                                                                                                                                                                                                                                                                                             roAspPheGlyPheGlyGlyGlnLysArgGlnLeuGluAspGlyAspGlnProAspSerL
                                                              lyCysLysValGlnIle---SerProAspSerGlyGlyLeuProGluArgSerValSerL
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1784	AGTGAGGCTCCCACAGGCACCAGCAAAACAACGGATGAATGTAGCCCTT	1736
538	roPheHisProGlyProPheAsnGlnGlyProProGlyAlaProProHisAlaGlyGlyP	518
1735	TCGCCTCACAGCGCAGCA-	1718
518	AAATTGTRCAACAGGTGAAGCAGCAGAGAAATHCCCILAGGAG	1670 498
498	rProGlnGlnIleAspHisAlaLysGlnLeuIleGluGluLysIleGlu	4.
1669	C.	1618
1617 480	TCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTC :::	1571 460
0 7	AAGTC heVal	1511 440
40	CCAAAGAAGAAGIGAAGCIGAAAGCGCATATCAAAGTGCCTT I CCAAAGCTGCCCGC 	1451 424
424	laProGlyMetProProGlyGlyArgGlyArgGlyArgGlyGlnGlyÅsnTrpGlyProP	404
1450	AACTTCTTAACC	1438
404	ProGlyProProGlyA	384
1437		
1408 384	ACGTCAGCGAAAGGATGGTCATCATCACCGGGCCACCGGAAGGCCCAGTTCAAGGCCCAGG	1349 366
1348 366	TCAAACAGCTGGCGAGATTCGCCGGAAGCCTCTATCAAGATTGCCCCTGCGGAAGGCCCAG :::	1289 3 4 6
346		1229 326
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N	GAGCAGGAGATTG	1175
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291	TCATCTTTGCAGGATTTGAGCATATTACACCCGGAAAGACCATCATGTGAAGG ::::::	1000
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschil S.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschil S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Jordan H., Moore T., Max., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 191-193; 203-206; 272-279; 284-290; 300-314; 321-328; 394-397; 409-411; 430-438 440-443, AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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10-CCT-2003 (Rel. 42, Created)
10-CCT-2003 (Rel. 42, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Far upstream element binding protein 1 (FUSE binding protein 1) (FBP)
(DNA helicase V) (HDH V).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Avigan M., Levens D.;
"A sequence-specific, single-strand binding upstream element of c-myc and defines a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genes Dev. 8:465-480(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94170991; PubMed=8125259; Duncan R., Bazar L., Michelotti G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=21127960; PubMed=11222755; Vindigni A., Ochem A., Triolo G.,
                                                           SEQUENCE OF 45-64; 133-145; 271-283; 308-321; 379-386;
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                                 PROSITE; PS50084; KH TYPE 1;
Transcription regulation; Transcription Repeat; Ubl con
                                                                               InterPro; IPR004088; Pfam; PF00013; KH; 4.
                                                                                     InterPro; IPR008160; Collagen.
InterPro; IPR004087; KH dom.
InterPro; IPR004088; KH_type_1.
                                                                                                                                                            EMBL; U05040; AAA17976.2; -. EMBL; BC017247; AAH17247.1;
                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Braddock D.T., Louis J.M., Baber J.L., Leve "Structure and dynamics of KH domains from single-stranded DNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22716800; PubMed=12819782; Kim H.J., Park B.-J., Kang Y.-S., Kim H.J., Park J.-H., Lee S.W., Han J.M., Lee H.-W., Kim S.; "Downregulation of FUSE-binding protein and c-myc by terestor p38 is required for lung cell differentiation. Nat. Genet. 34:330-336(2003).
                       3D-structure.
                                                                     SMART; SM00322; KH;
                                                                                                                               MIM; 603444;
                                                                                                                                            Genew;
                                                                                                                                                      PDB; 1J4W; 06-MAR-02
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PTM: Ubiquitinated. This targets
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MEDLINE=22388257; PubMed=12477932;
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Mammalia; Eutheria; Rodentia;
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Far upstream element binding protein 1 (FUSE binding protein 1)
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"Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                              both as activator and repressor of transcription SUBUNIT: Interacts with SIAHBP1/FIR and JTV1 (By SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                           FUNCTION: Regulates MYC expression by binding to a single-stranded far-upstream element (FUSE) upstream of the MYC promoter. May act both as activator and repressor of transcription (By similarity)
                                                                                                 Event=Alternative
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                            similarity).
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, Kiyosawa H.,
C., Gojobori T.,
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IsoId=Q91WJ8-2; Sequence=VSP_008322;

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DB:
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Transcription regulation; Trans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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InterPro; IPR004088; KH_type_1.
Pfam; PF00013; KH; 4.
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KH 4.

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Q92945; 000301; Q9UNTS; Q9UQHS;

10-CCT-2003 (Rel. 42, Created)

10-CCT-2003 (Rel. 42, Last sequence update)

10-CCT-2003 (Rel. 42, Last annotation update)

Far upstream element binding protein 2 (FUSE binding protein type splicing regulatory protein) (KSRP) (p75).
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"A new regulatory protein, KSRP, mediates exon intronic splicing enhancer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., SEQUENCE OF 72-85; 123-128; 348-359; 472-486; 488-492; 620-625; 627-644 AND TISSUE-Neuroblastoma, and Retinoblastoma; MEDLINE-97282621; PubMed-9136930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                             "The far upstream element-binding proteins comprise as of single-strand DNA-binding transactivators.";
J. Biol. Chem. 271:31679-31687(1996).
                                                                                                                                                                                                                                                                                                                                                                                                      "Mapping of the KHSRP gene to a region of conserved chromosome 19p13.3 and mouse chromosome 17."; genomics 56:350-352(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-115 AND 570-707 FROM N.A. MEDLINE=99189245; PubMed=10087204; Ring H.Z., Vameghi-Meyers V., Nikolic J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUBP2 OR KHSRP
                           Markovtsov V., Black D.L.;
                                                                                                                                                                                                                                                                                          TISSUE=B-cell lymphoma, and Skele
MEDLINE=97094955; PubMed=8940189;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Francke U.;
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                                                                                          MEDLINE=20459250;
                                                                                                                  FUNCTION,
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                                                                                                                  AND
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assembly of an hnRNP complex induced by
                                                                                                               INTERACTION WITH PTBP1;
                                                               Nikolic
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                                                            J.M.,
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                                                               Goldman J.A., Turck C.W.,
                                                                                                                                                                                                                                                                                                                           AND FUNCTION. celetal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   522
                                                                                                                           PTBP2 AND HNRPH1
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AND FUNCT
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뮹 5 US-09-270-437D-8

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(1-707)

104 cceccercacceaceaccrcceecaecrerrreseeacacaecaecaecrecccreece

proproGlyproProProProAlaGlyGlyGlyGlyAlaGly-GlyAlaGlyGlyGl

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Query
DB:
                       Best Local Similarity:
                                    Percent Similarity:
                                                                       Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MO1. Cell. Biol. 20:7463-7479(2000).

-i- FUNCTION: Binds to the dendritic targeting element and may play a role in mRNA trafficking (By similarity). Part of a ternary complex that binds to the downstream control sequence (DCS) of the pre-mRNA. Mediates exon inclusion in transcripts that are subject to tissue-specific alternative splicing. May interact with single-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/entities requires a license agreement (See http://www.isb-sib.ch/announce/
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EMBL; AF093745; AAD29861.1; JOINED.
EMBL; AF093748; AAD29862.1; -.
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                  SMART; SM00322; KH;
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                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:6316; KHSRP.
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U69126; AAC50892.1; ALT_FRAME
                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                             Transport; mRNA transport;
                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR004087; InterPro; IPR004088;
                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                    REPEAT
            Match:
                                                             No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and HNRPH1.
SUBCELLULAR LOCATION: Nuclear.
the cytoplasm of neuronal cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
TISSUE SPECIFICITY: Detected in neural and non-neural
SIMILARITY: Contains 4 KH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene expression.
SUBUNIT: Part of a ternary complex containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAUTION: Ref.3 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stranded DNA from the far-upstream element (FUSE). May activate
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233
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e differs fr
                                                                                                                                                                                                                                                                                                                               mRNA
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GLY-RICH.
ALA/GLY/PRO-RICH.
G-> V (IN REF. 2).
V -> G (IN REF. 2).
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                                                                                                 --> GG (IN REF. 2)
--> A (IN REF. 2)
E07588DE43BCA8B6
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-acting factor; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A small proportion is bodies and dendrites (
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Matches:
  Gaps:
                          Conservative: Mismatches:
                 Indels:
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2/2 SpG1ySerGlnAsnThrAsnValAspLysProLeuArgIleIleGlyAspProTyrLysV 292 1061 TTGAGGCCTGTGCCAGTGCTGAGATTAGAGATTATGAAGAAGCTGCGTGAGGCCTTTGAAA 1120 ::: ::: ::::::: ::::::: 292 alGlnGlnAlaCysGluMetValMetAspIleLeuArgAsnValThrLysAlaGlyPheG 312 1121 ATGATATGCTGGCTGTTAACACCCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACC 1180 312 lyAsp		862	746 GGGTAGATATCCATAGAAAAGAAACTCTGGAGGTGCAGAAAGCCTGTCACCATCCAT	143 hrserMetThrGluGluTyrArgValProAspGlyMetValG 157 686 GTGCCATCATCGGAAAGGAGGCCTTGACCATAAAGAACATCACTAAGCAGACCCAGTCCC 745		458 GAGAAGAAGAAATAGCCATGGAGAAGCTAAGCGGGCATCAGTTTGAGAACT 511		164 GACAGGTCCTGCTGAAGTCCGGGCTACGCCTTCGTGGACTACCCCGACCAGAACTGGGCCA 223
1954 CGAGCCCCGCCTCC	Qy 1843 CCATCTGAGGAATGAGAAGTCTGCGAGGCCAGGGACTCTGCCGAGGC 1893 Db 572 laAlaTrpAlaAlaTyrTyrSerHisTyrTyrGlnGlnProProGlyProValPro 590 Qy 1894 CCTGAGAACCCCAGGGGCCGAGGAGGGCGGGAAGGTCAGCCAGGTTTGCCAGAACCAC 1953 Qy 1894 CCTGAGAACCCCAGGGGCGGAGGGGGGGAAGGTCAGGCCAGGTTTGCCAGAACCAC 1953	QY 1777 FAGCCCTTRCCARCACCTGACAGAAIG	1661 492 1717 512	454 laPheValGluIleS 1613 TCGTCAGA ::: 474 leIleArgGlySerF	–	QY 1420	QY 1274 AGAAGGGGGACACATCAAACAGCTGGCGAGATTCGCCGGAGCCTCTATCAAGATTGCCC 1333	Qy 1181 AGTTTGGC

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                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., SEQUENCE OF 104-119; 242-267; 679-685; 705-711 I 743-766, FUNCTION, DEVELOPMENTAL STAGE, AND SUBCELLULAR LOCATION.
MEDLINE-21640447; PubMed-11781334;
Gu W., Pan F., Zhang H., Bassell G.J., Singer R.H.;
"A predominantly nuclear protein affecting cyroplasmic localization beta-actin mRNA in fibroblasts and neurons.";
J. Cell Biol. 156:41-52(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; (Archosauria; Aves; Neognathae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken)
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10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF461020; AAL66365.1; --
GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0003730; F:mRNA 3' UTR binding; IDA.
GO; GO:0003730; F:mRNA localization, intrac
                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00013; KH; 4. SMART; SM00322; KH; 4.
                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                  Transport;
                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_type_1.
                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                     No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell Biol. 156:41-52(2002).

FUNCTION: Binds to a 54-nucleotide localization signal (the FUNCTION: Binds to a 54-nucleotide region of beta-actin mRI zipcode) found in the 3' untranslated region of beta-actin mRI and may play a role in its localization.

SUBCELLULAR LOCATION: Predominantly nuclear. Also detected in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \overline{\text{DEVELOPMENTAL}} STAGE: The highest expression is embryos, is reduced to 30% before hatching and thereafter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 4 KH domains.
182
                          132
                                                                                                             160 ArgSerGlyProValGlyAspProProGlyProProArgAla
                                                                                                                                                                                                                          Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                PS50084;
                         GCTCTTTGGGGACAGGAAGCTGCCCCTGGCGGACAGGTCCTGCTGAAGTCCGGCTACGC
                                                                                 GATGAACAAGCTTTACATCGGGAACCTGAGCCCCGGCGGTCACCGCCGGACGACCTCCGGCA
                                                                                                                                       AGGCGAGGAGCGCCGGGTACCGGGGCCCGGGGAGCCGGGCTCTCGGGGAAGAGACGGAT
                                                                                                                                                                                                                                                                                                                                        mRNA
208
296
385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
ling protein 2.
                                                                                                                                                                                                                                                                                                              769
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                                                                                                                                                                                                                                                                                                                                                                                  4; KH_TYPE_1; transport; No
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259.00
36.73%
24.91%
4.40%
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Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                              80644 MW;
                                                                                                                                                                                                                                                                                                                                                                                   Nuclear protein;
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  -ThrGlyGlyAlaLeuProSer-
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                     RNA-binding; Repeat.
                                                         -GluArgGlyArgArgProProPro
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                                                                                                                                                                                                                                              eAspValProValProArgHisSer-----valGlyValVallieGlyArgSerGlyGl
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                                               TGTTAACACCCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGTTTGGCCCGTT 1193
                                                                                                                                 pAspGlyThr---GlyProGluLysIleAlaHisIleMetGlyProProGluArgCysGl
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RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Harris B., Ansorge W., Brandt P., Grivell L., Rieger M.,
RA Harris B., Ansorge W., Brandt P., Grivell L., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Vos P., Hoheisel J., Zimmernann M., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robsen J.,
Vandenbussche F.,
RA Langham S.-A., McCullagh B., Bilham L., Robsen J.,
Vandenbussche F.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirtse W.,
RA Mocijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercg R.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercg R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Polse S., de Haan M., Maarse A., Schaefer M., Meller-Auer S.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Neumann S., Argiriou A., Vitale D., Liguori R., piravandi E.,
RA Neumann S., Argiriou A., Vitale D., Liguori R., piravandi E.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid.
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Putative nucleic acid binding protein At4g18375.
AT4G18375 OR F28J12.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Columbia;
MEDLINE=20083488; PubMed=10617198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
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16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, L
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TEXES BERREADED

Hypothetical protein; Nuclear Alternative splicing.
DOMAIN 35 99 F

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Pfam; PF00013; KH; 5. SMART; SM00322; KH; 5.

InterPro; IPR004087; KH_dom. InterPro; IPR004088; KH_type_1.

PROSITE; PS50084; KH_TYPE

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protein;

RNA-binding; Repeat;

EMBL; AL021710; CAA16717.1; ALT SEQ. EMBL; AL161548; CAB78839.1; ALT SEQ. EMBL; AY133701; AAM91635.1; -. EMBL; BT001108; AAN64172.1; -.

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A Heijnen I., Schwarz S., Scholler I., Waller N., Stocker S., A Frishman D., Haase D., Lemke K., Mewes H.-W., Stocker S., A Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K., Ra Scharl L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L., Ra Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J., Sheet P., Courtes T., Harmon G., Edwards J., Constant P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., Ra Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., Ra Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K., K., Ra Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W., Ra Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D., Ra Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman C., Ra Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ra Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ra Ma P., Zhong J., Preston R., Vil D., Shekher M., Mattero A., Shah R., Ra Swaby I.K., O'Shaugnessy A., Rodriguez M., Hoffman J., Till S., Ra Granat S., Shohdy N., Hasegawa A., Haneed A., Lodhi M., Johnson A., "Commen." And analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
Xamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
"Empirical analysis of transcriptional activity in the Arabidopsis
use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome."
                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 302:842-846(2003).
-!- SUBCELLULAR LOCATION:
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Columbia;
MEDLINE=22954850; PubMed=14593172;
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                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 5 KH domains CAUTION: Ref.1 sequences differ from that shown
                                                                                                                                                                                                                    gene model prediction. At4g18370 and fused into a single gene.
                                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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                                   CysValIleIleValThrAlaThrGluSerProAspAspMetLysSerMetAlaValGlu
                                                                              CCTGTCACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATGATTCTTGAA
                                                                                                                  AAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCTGGAGCTGCAGAGAAG
                                                                                                                                                                                               CCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGAACATCACT
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/FTId=VSP 008899.
Missing (in isoform 2)
/FTId=VSP 008900.
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                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=20396135; PubMed=10936052;

Makeyev A.V., Liebhaber S.A.;

"Identification of two novel mammalian
of KH-domain RNA-binding proteins.";

Genomics 67:301-316 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                      -!- FUNCTION: Single-stranded nucleic acid binding preferentially to oligo dC (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- TISSUB SPECIFICITY: Ubiquitous.
-!- SIMILARITY: Contains 3 KH domains.
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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AlaLeuIleGlnIleValLeuArgLeuArgGluAspValLeuGlyAspLysAspSerVal 470
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Best Local Similari
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InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_type_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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HSSP; Q07244; 1KHM.
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SM00322; KH; 3.

E; PS50084; KH TYPE 1; 3.

x protein; RNA-binding; R
rIleProTyrArgProLysProAlaCysThrProValIlePheAlaGlyGlyGlnAlaTy
                                                                              CGTGAGGCCTTTGAAAATGATATGCTGGCTGTTAACACCCACTCCGGAT------
                                                                                                                                       ACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCTGAGATAGAGATTATGAAGAAGCTG
                                                                                                                                                                   AlaGlnValGlnValAlaGly-----AspMetLeuProAsnSerThrGluArgAlaVal
                                                                                                                                                                                              ACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATATACAACCCGGAAAGAACCATC
                                                                                                                                                                                                                         CysGlySerLeuileGlyLysGlyGlySerLysIleLysGluileArgGluSerThrGly
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                                                                                                             ThrIleSerGlyThrProAspAla-Ile-
                                                                                                                                                                                                                                                                               {\tt AsnSerProAlaThrSerLysProProValThrLeuArgLeuValValProAlaSerGln}
                                                                                                                                                                                                                                                                                                         GATGAGACCAAACTAGCCGAA---GAGATTCCTCTGAAAATCTTGGCACACAATGGCTTG
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Mismatches:
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Gaps:
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P57721;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                               InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_type_1.
Pfam; PF00013; KH; 3.
SMART; SM00322; KH; 3.
                                                                                                                             Genew; HGNC:8651; PCBP3.
GO; GO:0005634; C:nucleus; ISS.
GO; GO:0003677; F:DNA binding; ISS.
GO; GO:0003723; F:RNA binding; NAS.
GO; GO:0016671; P:mRNA metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of KH-domain RNA-binding proteins.";
Genomics 67:301-316(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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     PROSITE;
                                                                                                                                                                                                                                                                         EMBL; AF176329; AAG
HSSP; Q07244; 1KHM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -I- FUNCTION: Single-stranded nucleic acid binding preferentially to oligo dC (By similarity).
-I- SUBCELLULAR LOCATION: Nuclear (By similarity).
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MEDLINE=20396135; PubMed=10936052;
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16-OCT-2001 (Rel. 40, Last
16-OCT-2001 (Rel. 40, Last
Poly(rC)-binding protein 3
                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Makeyev A.V., Liebhaber S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                            an email to license@isb-sib.ch).
     PS50084; KH
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(See http://www.isb-sib.ch/announce/
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         GluLeuThrIleProAsnAspLeuIleGlyCysIleIleGlyArgGlnGlyThrLysIle
                                              AATCTCTTCATCCCAACCCAGGCTGTGGGCGCCATCATCGGGAAGAAGGGGGGCACACATC
                                                                                                                                               LeuGlyGlnThrAsnProAlaPheProGlyGluLysLeuProLeuHisSerSerGluGlu
                                                                                                                                                                                                                     HisProAspGlnLeuThrLysLeuHisGlnLeuAlaMetGlnGlnThrProPheProPro
                                                                                                                                                                                                                                                                                           ValIlePheAlaGlyGlyGln-----AlaTyrThrIleGlnGlyGlnTyrAlaIlePro
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RA Strausberg R.D., Collins F.S., Wagner L., Schemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length
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"NEDO human cDNa sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=20396135, PubMed=10936052;
Makeyev A.V., Liebhaber S.A.;
"Identification of two novel mammalian
of KH-domain RNA-binding proteins.";
Genomics 67:301-316(2000).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                          human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-:- FUNCTION: Single-stranded nucleic acid binding preferentially to oligo dC (By similarity).
-:- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22388257; PubMed=12477932;
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SEQUENCE
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GO; GO:0003677; F:DNA binding; ISS.
GO; GO:0003723; F:RNA binding; NAS.
GO; GO:0016077; P:mRNA metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF176330; AAG09241.1; -.
EMBL; AK023993; BAB14761.1; -.
EMBL; BC003308; AAH03008.1; -.
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InterPro; IPR004088; KH_type_1.
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                                                                  ATCAAACAGCTGGCGAGATTCGCCGGAGCCTCTATCAAGATTGCCCCTGCGGAAGGCCCA
                                                                                          LeuArgLeuVallleProAlaSerGlnCysGlySerLeuIleGlyLysAlaGlyThrLys
                                                                                                                                                                                                    GAGGCCTTTGAAAATGATATGCTGGCTGTTAACACCCACTCCGGATACTTCTCCAGCCTG
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  AsnSerThrGluArgAlaValThrValSerGlyValProAspAlaIleIleLeuCysVal
                        GACGTCAGCGAAAGGATGGTCATCATCACCGGGCCACCGGAAGCC---
                                                                                                               GTGAATCTCTTCATCCCAACCCAGGCTGTGGGCGCCATCATCGGGAAGAAGGGGGCACAC
                                                                                                                                                          TACCCCCATCACCAGTTTGGCCCGTTCCCGCATCATCACTCTTATCCAGAGCAGGAGATT
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RNA-binding; Ribonucleoprotein;
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Conservative:
Mismatches:
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  (See http://www.isb-sib.ch/announce/
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  STRAIN=S288c;
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PBP2 YEAST
P38151;
01-OCT-1994
                                                       Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                  01-OCT-1994
16-OCT-2001
                                                                                                                        PAB1-binding protein 2.
PBP2 OR YBR233W OR YBR1531.
SEQUENCE FROM N.A.
                                        NCBI_TaxID=4932;
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(Rel. 30, Last sequence up
(Rel. 40, Last annotation
                                                                                                                                                                                                                                                      STANDARD;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mangus D.A., Amrani N., Jacobson A.;
"Pbplp, a factor interacting with Saccharomyces cerevisiae poly(A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-1994)
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Scherens B., Vierendeels F
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SMART; SM00322; KH; 3.
PROSITE; P850084; KH TYPE 1; 3.
Nuclear protein; RNA-binding; R
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PIR; S46109; S46109.
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InterPro; IPR004088; KH_type_1.
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SUBCELLULAR LOCATION: Nuclear (Potential).
SIMILARITY: Contains 3 KH domains.
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                                   GlyValProGluArgIleValTyrValArgGlyThrCysAspAspValAlaLysAlaTyr
                                                                                                                             ATAAAGAACATCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCT
                                                                                                                                                                                     CTGCGGATCCTGGTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGCTTGACC
                                                                                                                                                                                                                   AlaAspSerHisSerAspAsnAspHisAspSerProAspAsnValProSerAspValHis
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GO: GO:0005737; C:cytoplasm; NAS.
GO: GO:0005634; C:nucleus; NAS.
GO: GO:0005634; C:nucleus; NAS.
GO: GO:0003623; F:RNA binding; IDA.
GO: GO:0003697; F:single-stranded DNA
GO: GO:0016071; P:mRNA metabolism; NA
InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_type_1.
Pfam; PF00013; KH; 3.
PROSITE; PS000322; KH; 3.
PROSITE; PS50084; KH_TYPE 1; 3.
PROSITE; PS50084; KH_TYPE 1; 3.
PNCLlear protein; RNA-binding; Ribonuc
                       Nuclear protess.
Phosphorylation; Repeat.
DOMAIN 175
DOMAIN 97 162
DOMAIN 279 343
 CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                  EMBL; X78137; CAA55016.1;
EMBL; U24223; AAA91317.1;
EMBL; Z29505; CAA82631.1;
HSSP; Q07244; 1KHM.
                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 22:959-964 (1994).

-!- FUNCTION: Single-stranded nucleic acid binding protein that bind preferentially to oligo dc.
-!- SUBCELLULAR LOCATION: Loosely bound in the nucleus. May shuttle between the nucleus and the cytoplasm.
-!- TISSUE SPECIFICITY: Abundantly expressed in skeletal muscle, thymus and peripheral blood leucocytes while a lower expression observed in prostate, spleen, testis, ovary, small intestine, heart, liver, adrenal and thyroid glands.
-!- FTM: PHOSPHORYLATED. THE NON-PHOSPHORYLATED FORM(S) EXHIBITED TH SIMULARITY: Contains 3 KH domains.
-!- CAUTION: There is probably a frameshift error in the nucleotide
                                                                                                                                                                                                                                          GK; Q15365; -
MIM; 601209;
                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aasheim H.-C., Loukianova T., Deggerdal A., Smeland "Tissue specific expression and cDNA structure of a encoding a nucleic acid binding [oligo(dC)] protein pre-mRNA binding protein K.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Lymphocytes;
MEDLINE=94203810; P
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EMBO J. 14:4357-4364(1995)
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MEDLINE-96016208; PubMed-7556077;
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"Identification of
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MEDLINE=95331278; PubMed=7607214;
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NCBI_TaxID=9606;
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 GGGGCACACATCAAACAGCTGGCGAGATTCGCCGGAGCCTCTATCAAGATTGCC---
                                                          CAGGAGATTGTGAATCTCTTCATCCCAACCCAGGCTGTGGGCGCCATCATCGGGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATATACAACCCGGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCT
                             GlnThrThrHisGluLeuThrIleProAsnAsnLeuIleGlyCysIleIleGlyArgGln
                                                                                                                                                                                                                                                                                                                                                        CTGGCTGTTAACACCCACTCCGGATACTTCTCCAGCCTG---
                                                                                                                                                                                                                                                                                                                                                                                  valLysGlnIleCysLeuValMetLeuGluThrLeuSerGlnSerProGlnGlyArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGAAAATTGAACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGC
                                                                                       GlyIleAspSerSerSerProGluValLysGlyTyrTrpAlaSerLeuAspAlaSerThr
                                                                                                                                                {\tt AsnGlnValAlaArgGlnGlnSerHisPheAlaMetMetHisGlyGlyThrGlyPheAlam}
                                                                                                                                                                                                        LeuAspAlaTyrSerIleGlnGlyGlnHisThrIleSerProLeuAspLeuAlaLysLeu
                                                                                                                                                                                                                                                                   AspArgCysSerAspAlaValGlyTyrProHisAlaThrHisAspLeuGluGlyProPro
                                                                                                                                                                                                                                                                                                                           MetThrIleProTyrGlnProMetProAlaSerSerProValIleCysAlaGlyGlyGln
                                                                                                                                                                                                                                                                                                                                                                                                                 GAGATAGAGATT-----ATGAAGAAGCTGCGTGAGGCCTTTGAAAATGATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                             {\tt ProAsnSerThrGluArgAlaIleThrIleAlaGlyValProGlnSerValThrGluCys}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysGluIleArgGluSerThrGlyAlaGlnValGlnValAlaGly-----AspMetLeu
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GlyAlaAsnIleAsnGluIleArgGlnMetSerGlyAlaGlnIleLysIl

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Query Match:
                                                                                                                                                                                                                                                                                                                       Score:
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                                                                                                                                                                                     US-09-270-437D-8 (1-3283) x PCB1_RABIT (1-356)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thiele B.J., Berger M., Huth A., Reimann I., Schwarz K., "Tissue-specific translational regulation of alternative 15-lipoxygenase mRNAs differing in their 3'-untranslated Nucleic Acids Res. 27:1828-1836(1999).

-i- FUNCTION: Single-stranded nucleic acid binding protei preferentially to oligo dC (By similarity).

-i- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          019048;
16-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; C:
Mammalia; Eutheria; Lagomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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HSSP; Q07244; 1KHM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nuclear protein; RNA-binding; Ribonucleoprotein; DNA-binding; Repeat.
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             GluvalGlySerileIleGlyLysLysGlyGluSerValLysArglleArgGluGluSer
                                                                                                 GlyValThrGluSerGlyLeuAsnValThrLeuThrIleArgLeuLeuMetHisGlyLys
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. 40, Last sequence update)
. 40, Last annotation updat
. protein 1 (Alpha-CP1) (hnR
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(Alpha-CP1) (hnRNP
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Q00341; Q9UCY3;

Q1-NOV-1997 (Rel. 35, Created)

Q1-NOV-1997 (Rel. 35, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

Vigilin (High density lipoprotein-binding protein)
  protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGAAAATTGAACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGC 1020
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                                                                                                                                                                                                                                                                   TTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAAGAGGAA 1437
                                                                                                                                                                                                                                                                                                                                                     GCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCACCGGGCCCACCGGAAGCCCAG 1395
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298 1278 278 1176

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Roberts S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length
RI Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                 Genew; HGNC:4
MIM; 142695;
                                                                                                                                                                                                                 muse by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See hor send an email to license@isb-sib.ch).
                    InterPro;
                                                                                                                                                                                     EMBL; M64098; AAA35962.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                   present in both the cytoplasm and the FEBS Lett. 382:330-334(1996).
-i- FUNCTION: APPEARS TO PLAY A ROLE IT MAY FUNCTION TO PROTECT CELLS
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Kugler S., Grunweller
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Vigilin contains a functional nuclear localisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning and expression of a cellular high density lipoprotein-binding protein that is up-regulated by cholesterol loading of cells."; J. Biol. Chem. 267:12131-12141(1992).
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GO:0005886; C:plasma membrane; TAS. GO:0008289; F:lipid binding; TAS. GO:0008203; P:cholesterol metabolism; erPro; IPR004087; KH dom. erPro; IPR004088; KH_type_1.
                                                                                                                                                                                                                                                              ween the Swiss Institute of Bioinformatics and the E
Buropean Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Nuclear and cytoplasmic SIMILARITY: Contains 14 KH domains.
                                                                                                                  A44125; A44125.
1VIG; 03-APR-96.
1VIH; 03-APR-96.
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ller A., Probst
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J., Bailey M.C.,
                                  TAS.
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DB:
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                                                                                                                                                    721 AACATCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCTGGAGCT
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                                                               ATTCTTGAAATCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTG
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                                                                                                                               GluIle---ArgAspLysPheProGluValIleIleAsnPheProAsp---
                                                                                                                                                                         LeuIleIleGluGlnArgPheHisArgThrIleileGlyGlnLysGlyGluArgIleArg
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                                                                                                                                                                                                                     {\tt GinAlaLysArgGluLeuLeuGluLeuAlaSerArgMetGluAsnGluArgThrLysAsp}
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id transport; Cholesterol
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STRAIN=BDIX; TISSUE=Cerebellum;
Knudsen A., Monstad S.E., Vedeler C.A.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                         RNA-binding
                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                  Mammalia; Eutheria;
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                                              "Nova-1, the paraneoplastic Ri antigen,
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(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
protein Nova-1 (Neuro-oncological ventral
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus
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"Role of Nova-1 in regulating alpha2N, a novel glycine receptor splice variant, in developing spinal cord neurons.";

J. Neurobiol. 52:156-165(2002).

-i-FUNCTION: Functions to regulate alternative splicing in neurons binding pre-mRNA in a sequence-specific manner to activate exor inclusion. It binds specifically to the sequence UCAUY (By similarity). Acts to regulate a novel glycine receptor alpha-2 chain splice variant (alpha-2N) in developing spinal cord.

-i- SUBCELLULAR LOCATION: Nuclear.

-i- SUBCELLULAR LOCATION: Nuclear.

-i- SUBCELLULAR CONTAINS 3 KH domains.
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InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_type_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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SMART; SM00322; KH;
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Nuclear protein; RNI
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                                                                                                                                      LeuIleGlnGlyThrIleGluAlaLeuAsnAlaValHisGlyPheIleAlaGluLysIle
                                                                                                                                                                                     ACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATGATTCTTGAAATCATG
                                                                                                                                                                                                                                      \verb|AlaThrIleLysLeuSerLysAspPheTyrProGlyThrThrGluArgValCys|
                                    ArgGluMetProGlnAsnValAlaLysThrGluProValSerIleLeuGlnProGlnThr 139
                                                                                        CAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTG----
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CCCTCAGGGAGTC 1719 rGluGlnGlyVal 473	GACTGCACAGCGCAAGATC 1665	AAACGCCAGATGAAAATGAG 1605 	CGTGAACGAACTGCAGAAC 1551 :::	CATATCAGAGTGCCC 1491	AAGAAGTGAAGCTGGAAGCG 1476 ::: erProLeuAlaAlaSerAla 384	1422 neAlaLeuGlySerLeuAla 364	GGCCACCGGAAGCCCAGTTC 1398 yrAlaSerGluAla 344	CTATCAAGATTGCCCCTGCG 1338	yrGlyTyrAsnLeuAsnThr 306	1308	1308 erGlyPheThrGlyAsnAsp 286	ATCATCGGGAAGAAGGGG 1281 :::::: lyLeuLeuGlyHis 266	TCTTATCCAGAGCAGGAG 1224 ::: roThrGlyPheProTyrAlaAsn 249	GATACTTCTCCAGCCTGTAC 1170 	TTATGAAGAAGCTGCGTGAG 1110 :::::: ::::: eileGlnLysIleGlnGlu 218	CGGAAAGAACCATCACTGTG 1050 InGluargValValThrVal 198	AACATGAAACAGGGACCAAG 990 :::::: etGluGlnSerGlyAlaTrp 179		CACACAATGGCTTGGTTGGA 930

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-Q=/cgn2 1/USPTO_spool_p/US09270437/runat_23072004_095739_27425/app_query.fasta_1.5582
-DB=SPTREMBL_25 -QEFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LGOPEXT=0
-UNITS=bits -START=1 -RND=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pto -NORM=ext -HEAPSIZE=550 -MINLEN=0 -MAXLEN=2000000000
-USER-US09270437 @GCN_1 1_287 @runat_23072004_095739_27425 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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ALIGNMENTS

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RESULT 1

Q9Y6M1

D9Y6M1

PRELIMINARY; PRT; 556 AA.

AC Q9Y6M1;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 25, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 25, Last annotation update)

DF 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DF 0203 (TrEMBLrel. 25, Last annotation update)

DF 62:

CN P62:

CN Homo sapiens (Human).

CN Homo sapiens (Human).

CN Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

CN MAMMALIA; Butheria; Primates; Catarrhini; Hominidae; Homo.

CN NCBL_TAXID=9606;

EN [1]

RP SEQUENCE FROM N.A.

RS SEQUENCE FROM N.A.

RY MEDLINE=92207072; PubMed=10190901;

RA Zhang J.Y., Chan E.K., Peng X.X., Tan E.M.;

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RA Zhang J.Y., Chan E.K., Peng X.X., Tan E.M.;

RA Zhang J.Y., Chan E.K.
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Alignment s Pred. No.: Score:

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Percent Similarity:
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InterPro; IPR004088; KM_type_1.
InterPro; IPR004088; KM_type_1.
InterPro; IPR000504; RNA_rec_mot.
pfam; pF00013; KH; 4.
Pfam; pF00076; rrm; 2.
Pfam; pF00076; rrm; 2.
SMART; SM00322; KH; 4.
SMART; SM00360; RRM; 2.
PROSITE; PS50084; KH_TYPE_1; 4.
PROSITE; PS50102; RRM; 2.
PROSITE; PS50102; RRM; 2.
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Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chc
Mammalia; Eutheria; Rod
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RC STRALN=C57BL/6; TJSUB=Brain;

RC STRALN=C57BL/6; TJSUB=Brain;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Schaefer C.F., Bhat N.K.,

RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Diatchenko L., Marusina K., Farmer G.J., Abramson R.D., Mullahy S.J.,

RA Stapleton M., Oquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Robert S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

RA Willialon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Robert S.J., Marra M.A.,

RA Robert S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

"The Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column of the Column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-2003) to the EMBL; BC054552; AAH54552.1; Hypothetical protein. SEQUENCE 545 AA; 59679 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
GGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGATGAAGAGGTGAGC
                                                          GTTGTCAACGTCACATATGCAACAAGAAGAAGCAAAAATAGCCATGGAGAAGCTAAGC
                                                                                                                                                          GTGGAATTGCATGGGAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAGCTAAGGAGC
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Conservative:
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CUTT. SIMILARITY: CONTAINS 4 KH DOMAINS.

EMBL; AF066434; AAC18598.1; -.

EMBL; AF06523; AAC41285.1; -.

R GO; GO:003676; F:nucleic acid binding; IE:

R GO; GO:003676; F:nucleic acid binding; IE:

R InterPro; IPR004088; KH type.1.

R InterPro; IPR000504; RNA_rec_mot.

Pfam; PF00013; KH; 4.

DR SMART; SM00360; RRM; 2.

DR SMART; SM00360; RRM; 2.

DR SMART; SM00360; RRM; 2.

DR PROSITE; PS50102; RRM; 2.

DR PROSITE; PS50102; RRM; 2.

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O1-AUG-1998 (TrEMBLrel. 07, Created)
O1-AUG-1998 (TrEMBLrel. 07, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
VG1 RNA binding protein variant D.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Yenopodinae; Xenopus.
NCBI TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Havin L., Git A., Elisha Z., Oberman
Pressman Schwartz S., Standart N.M.,
Genes Dev. 0:0-0(1998).
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PROSITE;
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98228351; PubMed=9560341;
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                                                                                                                                                             TTCGTGGACTACCCCGACCAGAACTGGGCCATCCGCGCCATCGAGACCCTCTCGGGTAAA
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GTTGTCAACGTCACATATGCAACAAGAAGAAGAAGCAAAAATAGCCATGGAGAAAGCTAAGC
                                                                                                                  GTGGAATTGCATGGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAGCTAAGGAGC
                                                                                                                                               ATGAACAAGCTTTACATCGGGAACCTGAGCCCCGCCGTCACCGCCGACGACCTCCGGCAG
                                         TTGGCTCAATATGGGACAGTGGAGAATGTGGAACAGACACACAGACACAGAAAACCGCC
                                                                  ArgLysLeuGlnIleArgAsnIleProProHisLeuGlnTrpGluValLeuAspSerLeu
                                                                               ValGluLeuHisGlyLysValIleGluValGluHisSerValProLysArgGlnArgSer
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                              lnTyrGlyThrValGluAsnCysGluGlnValAsnThrGluSerGluThrAla
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78.50%
66.21%
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EMBL; AF042353; AAB97457.1; -
EMBL; AF064633; AAC18597.1; -
GO; GO:0003676; F:nucleic acid binding; II
InterPro; IPR004087; KH dom.
InterPro; IPR004087; KH type_1.
InterPro; IPR004088; KH_type_1.
InterPro; IPR004084; RNA_rec_mot.
Pfam; PF00013; KH; 4.
                                                                                       Pfam; PR00076; rrm; 2.
SMART; SM00362; RH; 4.
SMART; SM00360; RRM; 2.
SMO0360; RRM; 2.
PROSITE; PS50084; KH TYPE_1; 4.
PROSITE; PS50102; RRM; 2.
PROSITE; PS000102; RRM RNP 1; FA
SEQUENCE 593 AA; 65385 MW;
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"Characterization of a Xenopus oocyte
developmentally regulated cis-element
Dev. Biol. 151:306-316(1992).
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057526;
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Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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O1-JAN-1998 (TrEMBLrel. 05, 0
O1-JAN-1998 (TrEMBLrel. 05, 1
O1-OCT-2003 (TrEMBLrel. 25, 1
Zipcode-binding protein.
ROSS A.F., Oleynikov Y.S., Kislauskis E.H., Taneja K.L., Singer R.H.;

"Characterization of a beta-actin mRNA zipcode-binding protein.";

Mol. Cell. Biol. 17:2158-2165 (1997).

-!- SIMILARITY: CONTAINS 4 KH DOMAINS.

EMBL; AF026527; AAB82295.1; --

GO; GO:0003676; F:nucleic acid binding; IEA.

InterPro; IPR004088; KH dom.

InterPro; IPR004088; KH type_1.

InterPro; IPR004088; KNA_rec_mot.

Pfam; PF00013; KH; 4.
                                                                                                                                                                                                                                     ZBP1.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                        Archosauria; Aves;
                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=97220007; PubMed=9121465;
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; Galliformes; Phasianidae; Phasianinae;
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smarr; sm00322; KH; 4.
smarr; sm00350; RRM; 2.
pr051TE; PS50084; KH TYPE_1; 4.
pr051TE; PS50102; RRM; 2.
pr051TE; PS50102; RRM; 2.
pr051TE; PS50030; RRM RMP 1; FALSE NEG.
pr051TE; PS60030; RRM RMP 1; FALSE NEG.
seQUENCE 576 AA; 63271 MW; 01AAF2D1D81C8811
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US-09-270-437D-8
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InterPro; IPR004088; KH type 1.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PP00013; KH; 4.
Pfam; PF00076; rrm; 2.
SMARI; SM00322; KH; 4.
SMARI; SM00360; RRM; 2.
PROSITE; PS50048; KH TYPE 1; 4.
PROSITE; PS50102; RRM; 2.
SROSITE; PS50102; RRM; 2.
SEQUENCE 577 AA; 63436 MW; 064:
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STRAIN=Sprague-Dawley;
Eom T., Singer R.H., Bas
"Molecular interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transport of mRNA and stimulation of spine growth.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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[1]
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                                                                                          TCCCCTTCGCCCCCTCAGCGAGCCCAGCGTGGGGACCACTCTTCCCGGGAGCAAGGCCAC
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ileileGlyHisPheTyrAlaSerGlnMetAlaGlnArgLysileArgAspIleLeuAla
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RX MEDILINE-21085660; PubMed=11217851;
RA Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Komon H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Komon H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Sibabata Y., Storch K.-F.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=97322234; PubMed=9178888;
Leeds P., Kren B.T., Boylan J.M., Betz
Gruppuso P.A., Ross J.;
"Developmental regulation of CRD-BP, au
stabilizes c-myc mRNA in vitro.";
Oncogene 14:1279-1286(1997).
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01-CCT-2003 (TREMBLTel. 25, Last annotation update)
Coding region determinant binding protein.
IGF2BP1 OR CRDBP.
Mus musculum '...
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Genes Dev.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herrick D.J., Ross J.;
"The half-life of c-myc mRNA in growing and infilence of the coding and 3' untranslated ribosome translocation.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ross J., Prokipcak R.D., Fleisig A.J.;
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MEDLINE=92217743; PubMed=1559612;
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STRAIN=C57BL/6J; TISSUE=Embryo;
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l of c-myc mRNA half-life in vitro by a prot
to a coding region stability determinant.";
ev. 6:642-654(1992).
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SMART; SM00362; KH; 4.
SMART; SM00360; RRM; 2.
PROSITE; PS50084; KH TYPE_1; 4.
PROSITE; PS50102; RRM; 2.
SEQUENCE 577 AA; 63450 MW; 1
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"ENELTY: CONTAINS 4 KH DC EMBL; AR061569, AAC72743.1; --
EMBL; AK013940; BAB29071.1; --
HSSP; P11940; ICVU.
MGD; MGI:1890357; Igf2bp1.
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Q9NZI8;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HSSP; P11940; 1CVJ.
GOS, GO:0003676; F:nucleic acid binding;
InterPro; IPR004087; KH dom.
InterPro; IPR004088; KH_type_1.
InterPro; IPR000504; RNA_rec_mot.
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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: CONTAINS 4 KH DOMAINS.
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Pfam; PF00076; rrm; 2.
SMART; SM00322; KH; 4.
SMART; SM00360; RRM; 2.
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PROSITE; PS50102; RRM; 2.
SEQUENCE 577 AA; 63456 MW;
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"Analysis of the mouse transcriptome based on functional ann
fo,770 full-length cDNAs.";

I Nature 420:563-573 (2002).

R MGD; MGI:1890357; BAC32119.1; -.

R MGD; MGI:1890357; Igf2Dp1.

R GO: GO:0003676; F:nucleic acid binding; IEA.

RINTETPTO; IPR004087; KH dom.

RINTETPTO; IPR004088; KH-type_1.

R InterPTO; IPR004088; KH-type_1.

R InterPTO; IPR004088; KH-type_1.

R InterPTO; IPR004088; KH-type_1.

R INTETPTO; IPR004088; KH-type_1.

R Pfam; PF00013; KH; 4.

R Pfam; PF00013; KH; 4.

R Pfam; PF00076; xrm; 2.

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R SMART; SM00360; RRM; 2.

R PFAM; SM00322; KH; 4.

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                                                                                                                                                                                                                      RC STRAIN=129/SV x 129/SV-CP; TISSUB=Embryonic stem cells;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Schemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Rodriguez S., Worley M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez S.T. Marra M. A.
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01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                        STRAIN=129/Sv x 129/Sv-CP; TISSUE=Embryonic stem cells; Strausberg R.;
                                                                                                                                                   Jones S.J., Marra M.A.;
"Generation and initial analysis
and mouse cDNA sequences.";
                                                                                SEQUENCE FROM N.
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InterPro; IPR004087; KH dom
InterPro; IPR004088; KH typ
InterPro; IPR000504; RNA_re
Pfam; PP00013; KH; 4.
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SWART; SM00350; RRM; 2.
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PROSITE; PS50084; KH TYPE_1; 4
PROSITE; PS50102; RRM; 2.
SEQUENCE 577 AA; 63378 MW;
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                                        GCTGCAGAGAAGCCTGTCACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGC
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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,

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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gav J.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay J.J., Hulyk S.W.,

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RA Richards S., Worley K.C., Hale S., Sarcia A.M., Gay J.J., Hulyk S.W.,

RA Rahey J., Halton E., Ketteman M., Madon A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rahesley J., Marra M.A.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA "Generation and initial analysis of more than 15,000 full-length human

RT "Generation and initial analysis of more than 15,000 full-length human
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EMBL; AP161270; AAD45610.1; -
EMBL; BC045873; AAH45873.1; -
ZFIN; ZDB-GENE-000308-1; dvrlxbp
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MGD; MGI:1890359; Igf2bp3.
GO; GO:0003676; F:mucleic acid binding;
InterPro; IPR004087; KH dom.
InterPro; IPR004088; KH_type_1.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                             the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL, AK088465; BAC40370.1;
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[1]
SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE=Thymus;
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                  ArgGlnAla-----SerProGlySerValSerLysGlnLysProCysAspLeuProLeu
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Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 25, Last annotation update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Rodentia;
                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackembush J., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackembush J., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA Brownstein M.J., Balt C., Fletcher C., Fujita M., Gariboldi M., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., RA Syzuki H., Toyo-oka K., Mang K.H., Weitz C., Whittaker C., Wilming L., RA Havsahizaki Y.;
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RX MEDLINE=2238825; PubMed=12477932;
RX MEDLINE=2238825; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Iu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Altschaff M. I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
RA Fares S. T. Marya M. A.
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Yuasa Y., Takeda M., Okano H.;
"Expression of mouse igf2 mRNA-binding protein
for the developing central nervous system.";
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                                                                                                                  MGD; MGI:1890359; IG£2bp3.

GO; GO:0003676; F:nucleic acid binding;

InterPro; IPR004088; KH_type 1.

InterPro; IPR004088; KH_type 1.

InterPro; IPR000504; RNA_rec_mot.
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EMBL; BC049082; AAH45082.1; --
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6; TISSUE=Brain, and Olfactory epithelium;
                         SMART; SM00322;
SMART; SM00360;
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              SerIleLeuGluIleMetHisLysGluAlaGlnAspIleLysPheThrGluGluIlePro
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Eukaryota; Metazoa;
Mammalia; Eutheria;
  SEQUENCE FROM N.A. Mueller-Pillasch F., Oncogene 0:0-0(0).
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NA binding protein
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Primates;
                 Lacher
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n KOC
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                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
              Wallrapp
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(KOC).
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EMBL; U76705; AAD09223.1; ---
GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0005737; F:RNA binding; TAS.
GO; GO:0007345; P:embryogenesis and morpho
GO; GO:0006412; P:protein biosynthesis; TA
GO; GO:0006396; P:RNA processing; TAS.
InterPro; IPR004087; KH_dom.
InterPro; IPR004087; KH_dom.
InterPro; IPR004087; KH_type_1.
InterPro; IPR0050504; RNA_rec_mot.
Pfam; PF00013; KH; 4.
Pfam; PF00016; rrm; 2.
SMART; SM00322; KH; 4.
SMART; SM00350; RRM, RNP_T; 1; 4.
PROSITE; PS50084; KH_TYPE_1; 4.
PROSITE; PS50084; KH_TYPE_1; 4.
PROSITE; PS500030; RRM, RNP_T; FALSE NEG.
SEQUENCE 579 AA; 63720 MW; AE5C3A8EE3C
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: CONTAINS 4 XH DOMAINS.
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SEQUENCE FROM
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             GlnGlnAsnProLeuGlnGlnProArgGlyArgArgGlyLeuGlyGlnArgGlySerSer
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ATATACAACCCGGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCT
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ATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCAGGGAAATTGTACAA 1680
                                                                                    GCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTCAGA 1620
                                                                                                                                                                          AlaGlyArgValIleGlyLysGlyGlyLysThrValAsnGluLeuGlnAsnLeuSerSer
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EMBL; BT001739; AAN71494.1; -.
FlyBase; FBgn0030235; Imp.
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR004087; KH dom.
InterPro; IPR004088; KH_type_1.
Pfam; PF00013; KH; 4.
SMART; SM00325; KH; 4.
PROSITE; PS50084; KH TYPE_1; 4.
SEQUENCE 580 AA; 63407 MW; 86EA1F5D64523C02
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Celniker S.;
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Q8IGK4;
01-MAR-2003
01-MAR-2003
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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Stapleton M.,
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| AspLeuGluLeuSerLysGluAspArgGlu-
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                                                                      GGGGACCACTCTTCCCGGGAGCAAGGCCACGCCCCTGGGGGCACTTCTCAGGCCAGACAG
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                                                                                                                                                                                                                                                                                                                               GAACAAGTCAACACAGACAGAAACCGCCGTTGTCAACGTCACATATGCAACAAGAGAA
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ACCAAC ThrLys	ACC Thr
GTTGGA ::: IleGly	25 GTT ::: 83 Ile
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TCTGAAGCATGCCGCATGAT: ::: ::: ThrAsnAlaCysLysArgIle	43
AAAGAO LysGlu	23
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Search completed: July 23, 2004, 11:15:36 Job time: 192.961 secs

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